

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

FIG. 1

HPP-CFC (Colony #)

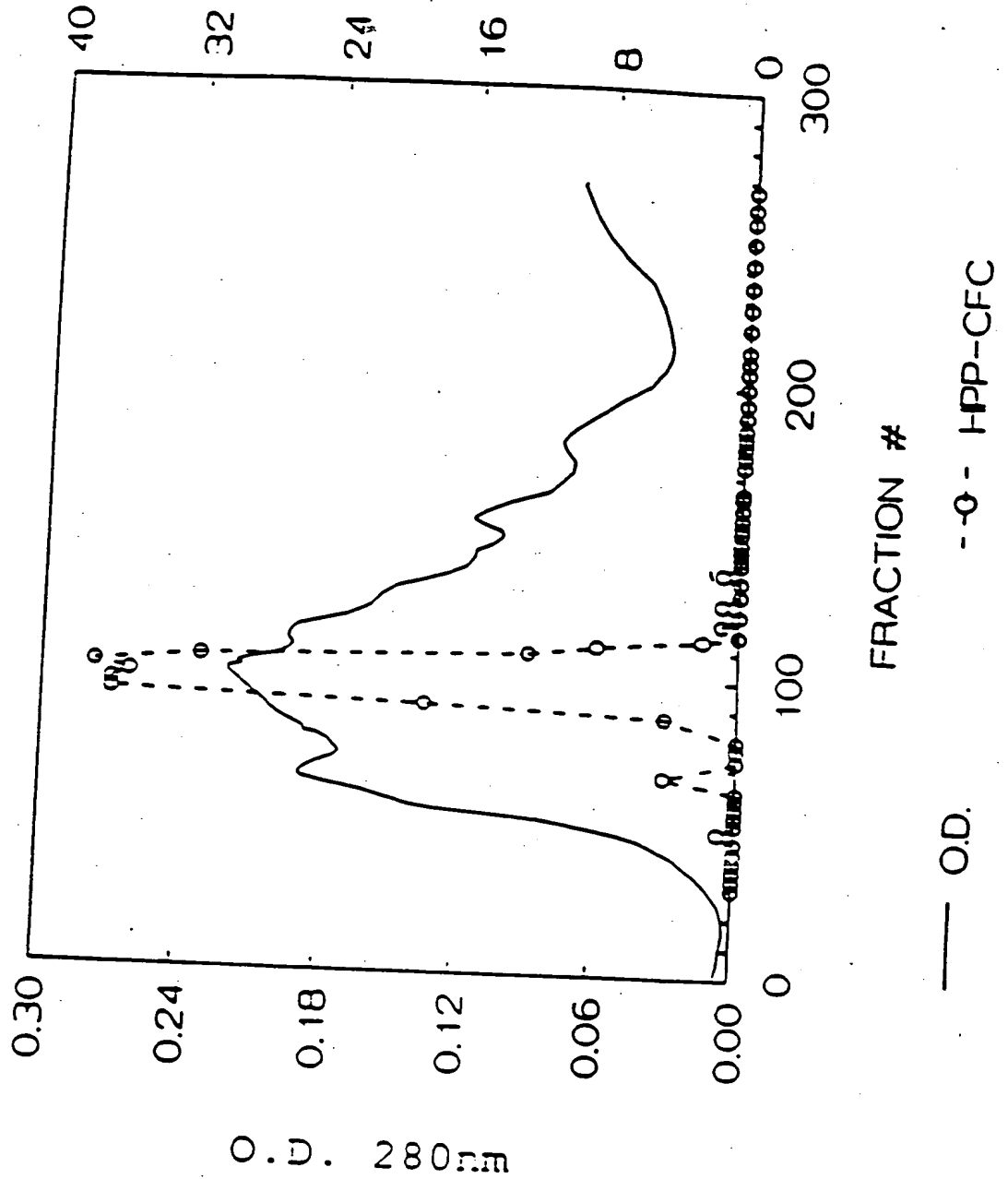


FIG. 2

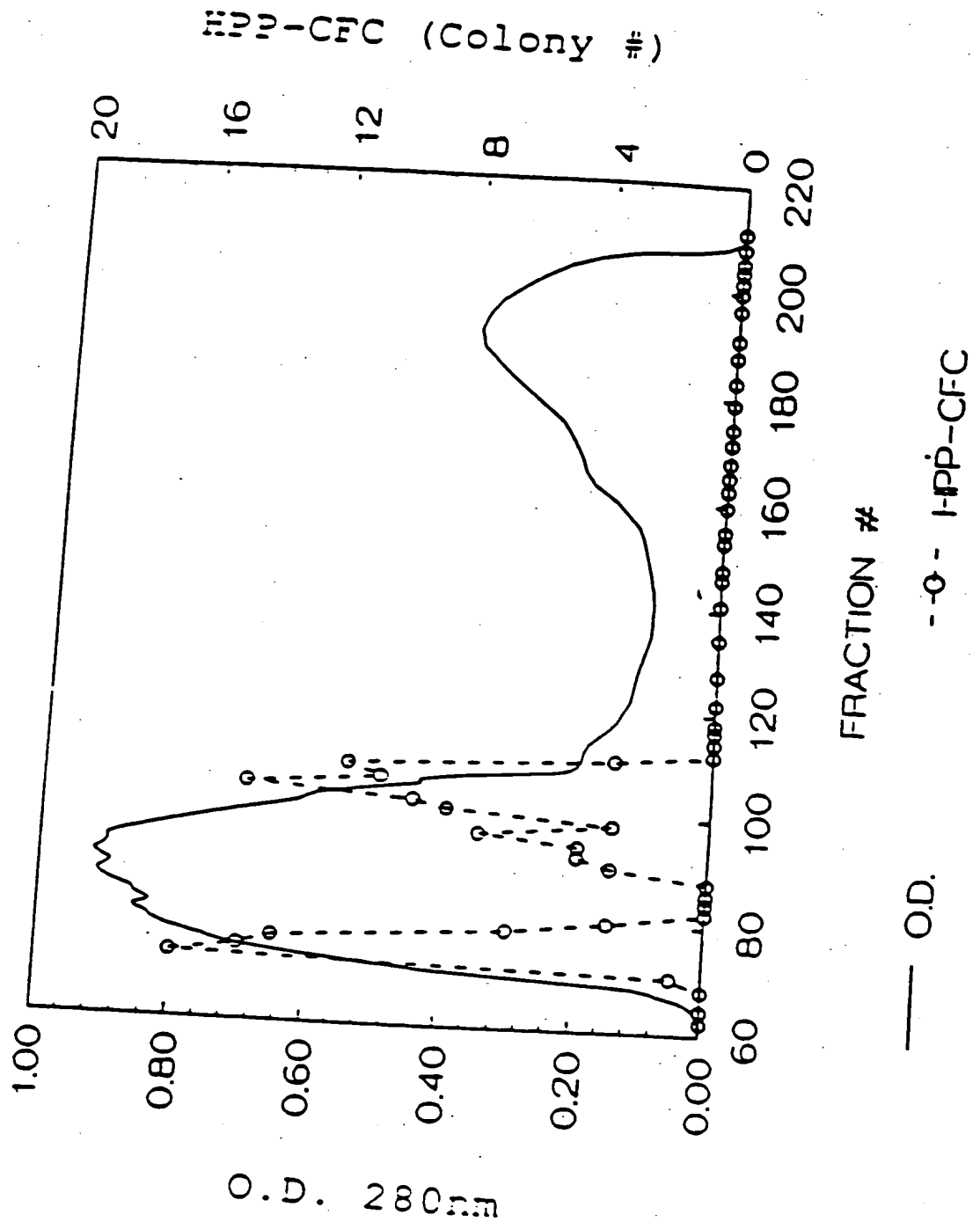


FIG.3

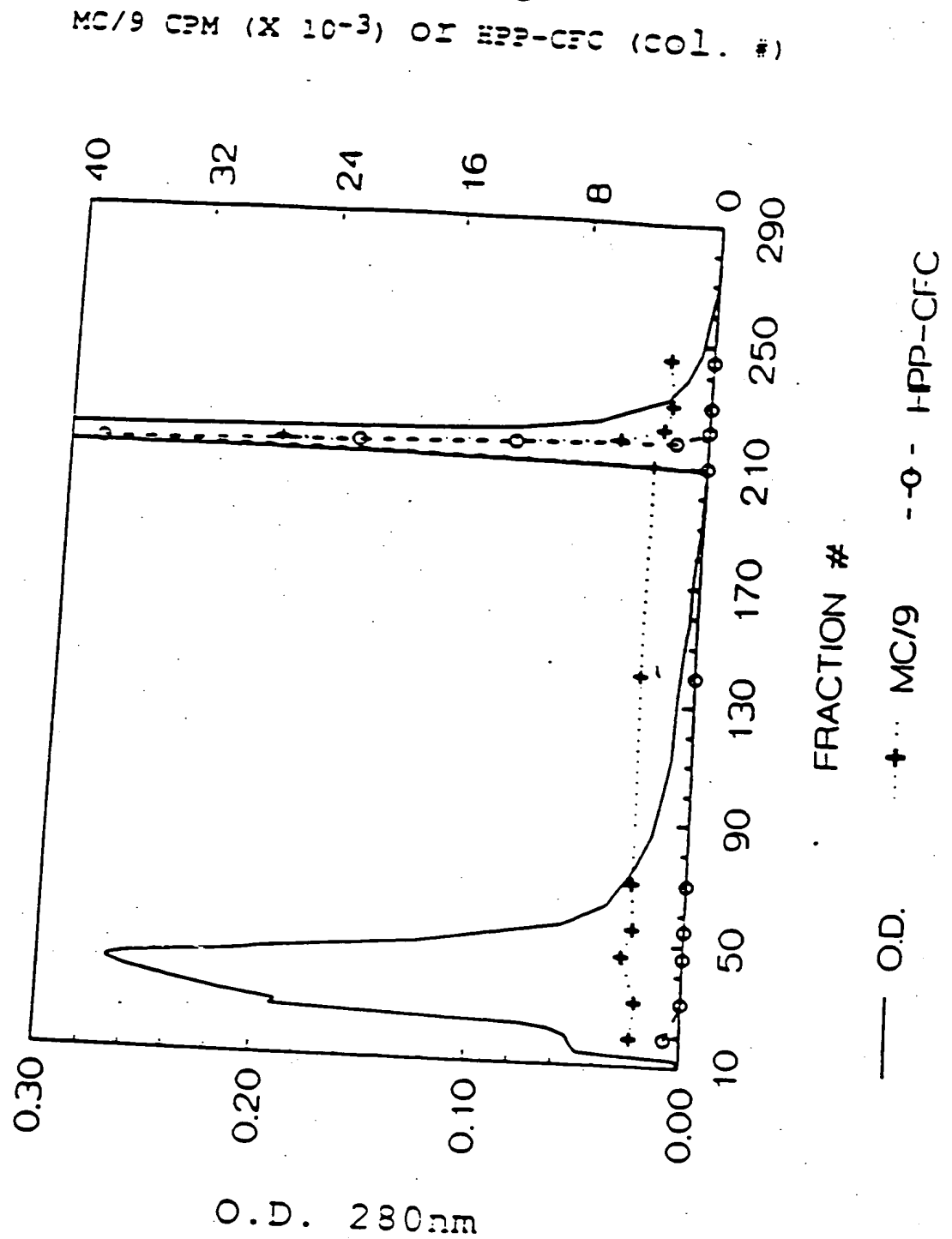


FIG. 4

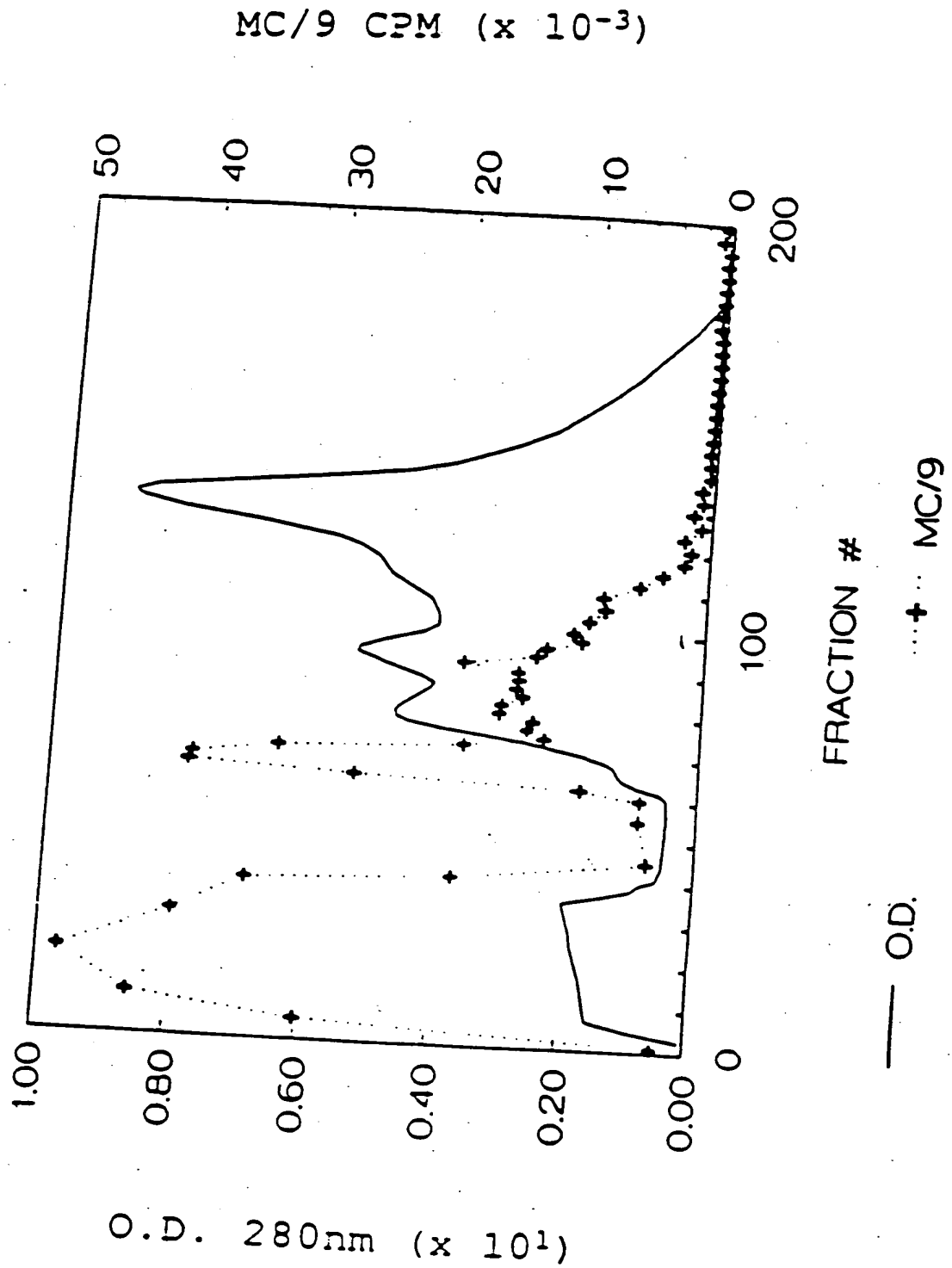


FIG.5

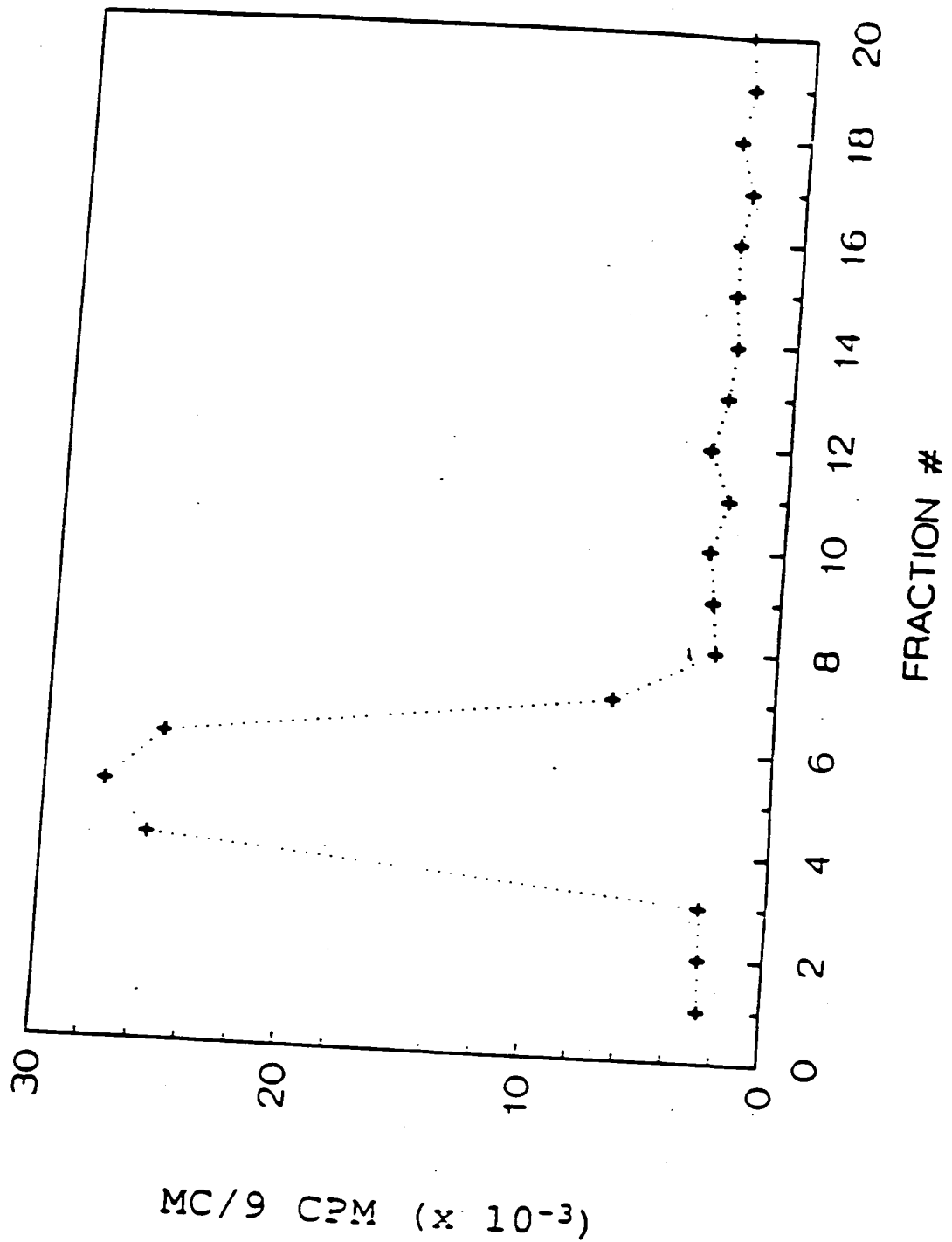


FIG. 6

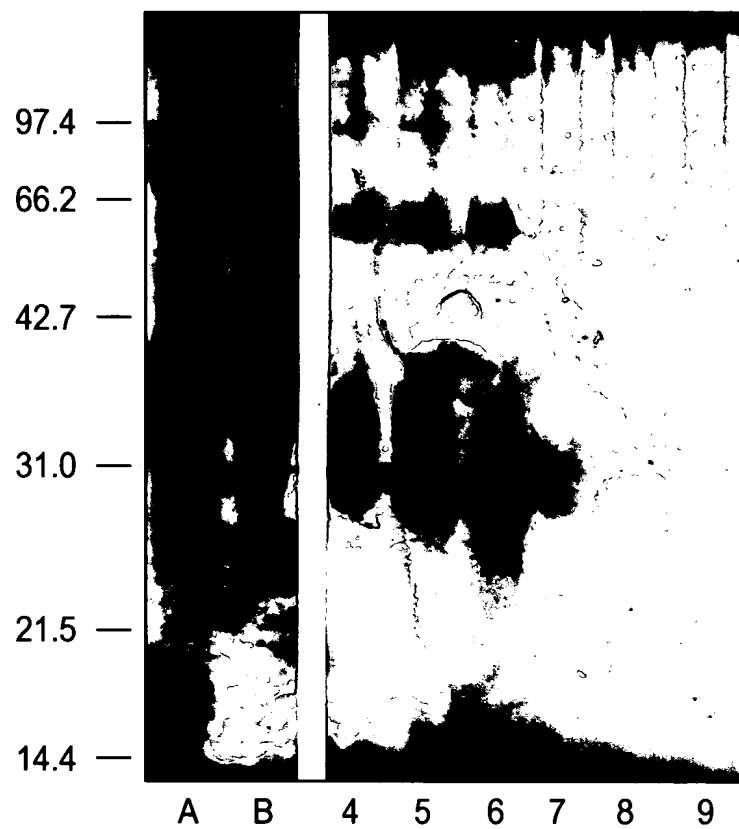


FIG. 7

MC/9 CPM

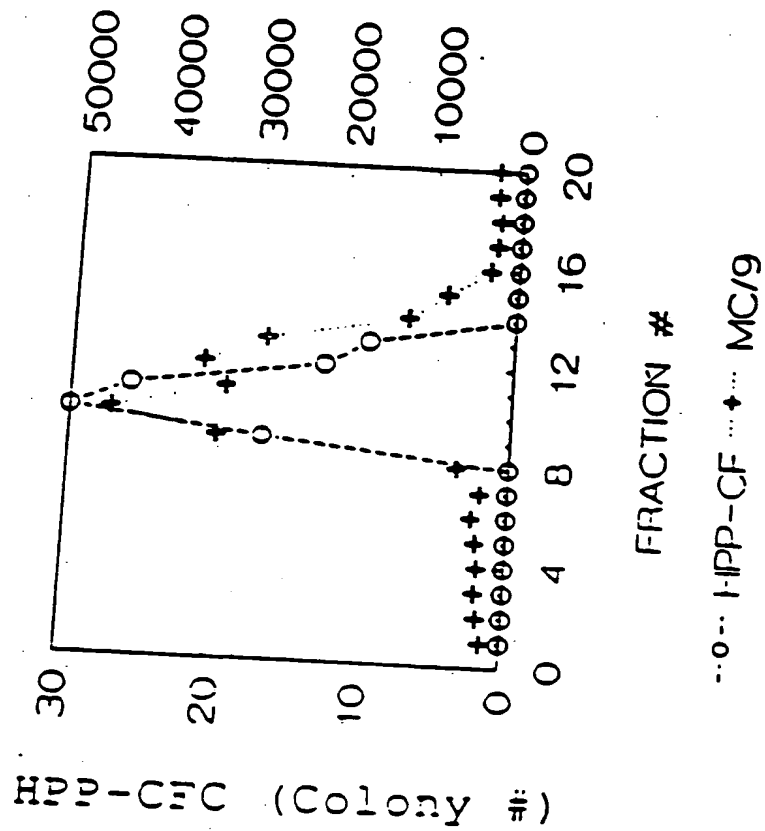


FIG. 8

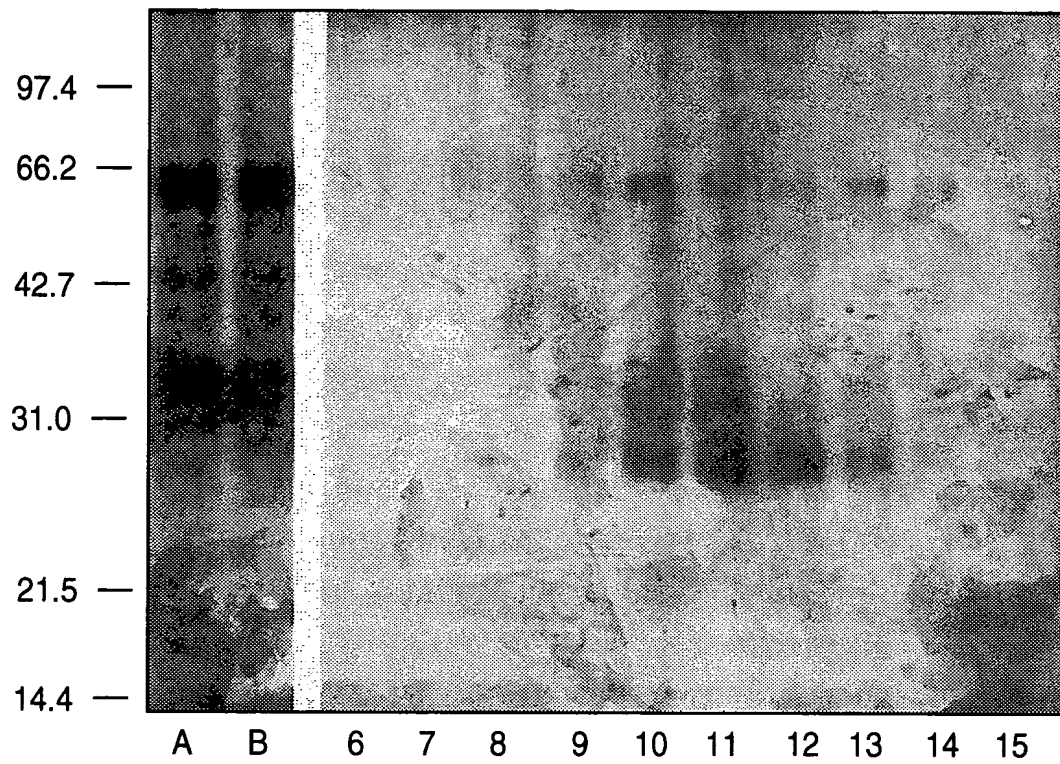


FIG. 9

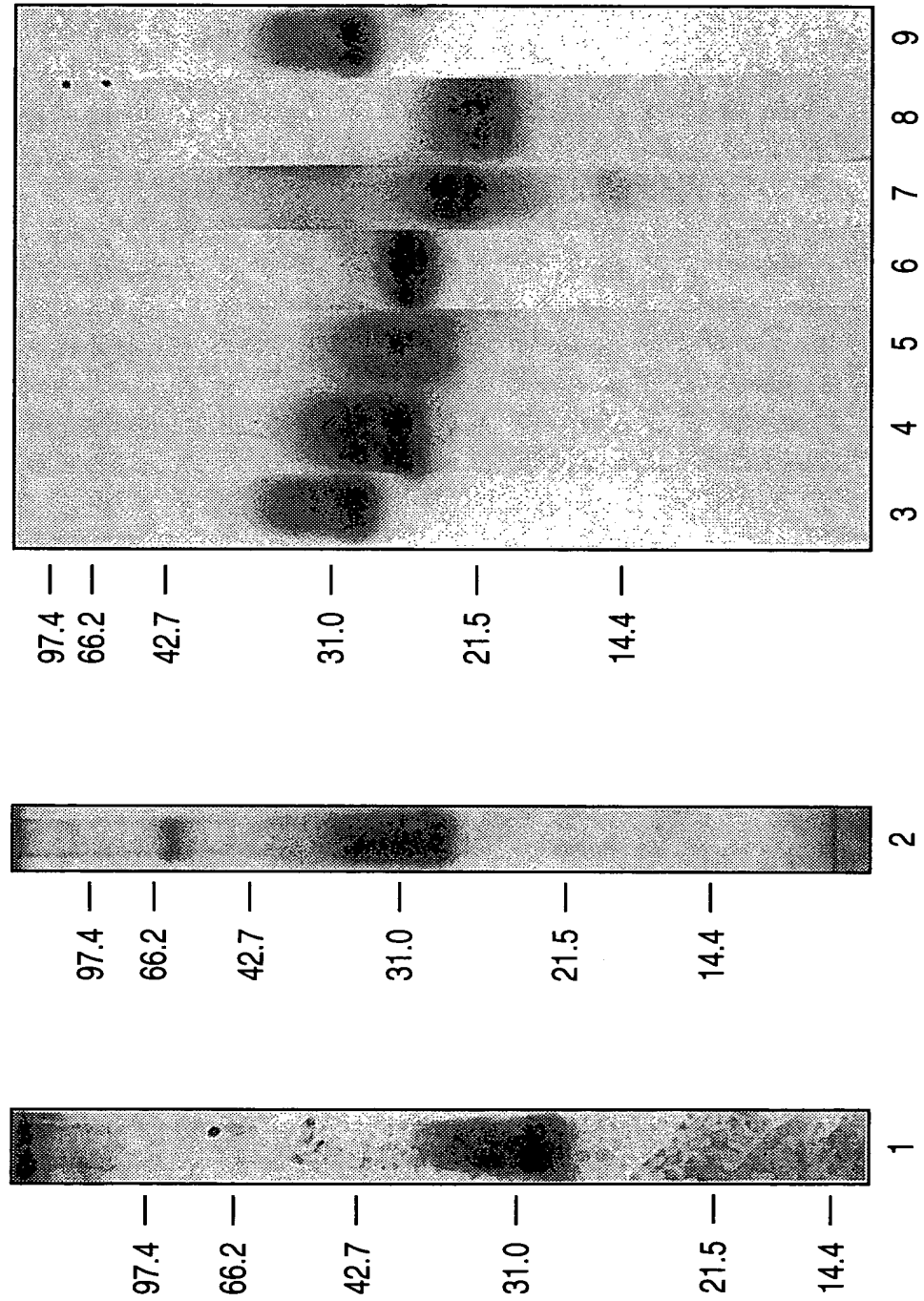


FIG.10

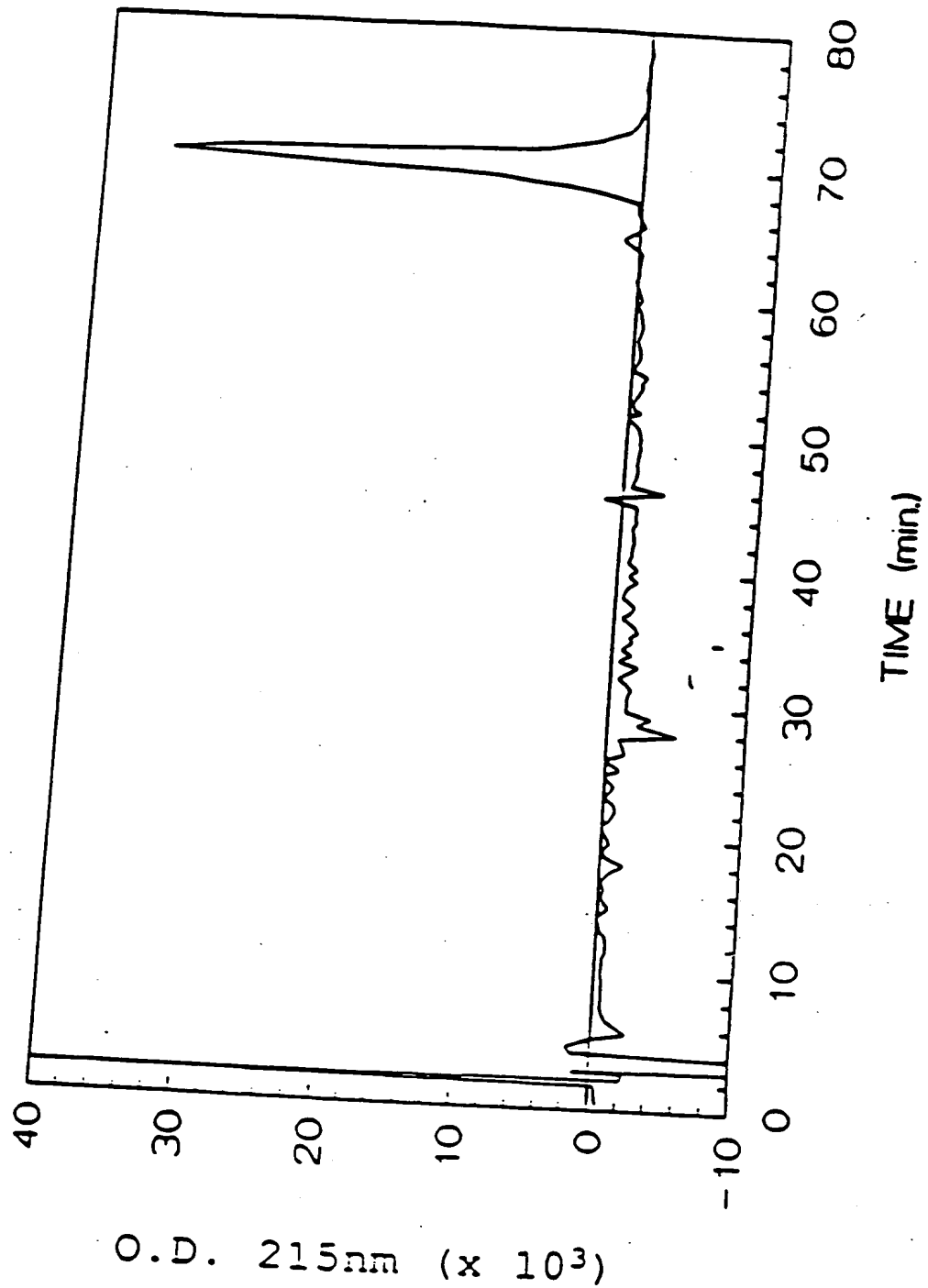


FIG. 11

1 10 20
pE E I C R N P V T D N V K D I T K L V A N L P N D
----- Sequencing after -----
----- T-5a -----
30 40 50
Y M I T L N Y V A G M D V L P S H C W L R D M V T
<Glu Aminopeptidase Treatment ----->
----- T-5a -----
----- CB-6a ----- CB-8; CB-10 -----
60 70
H L S V S L T T L L D K F S N I S E G L S N Y S I
----- Sequencing after Trp Cleavage -----
80 90 100
I D K L G K I V D D L V A C M E E N A P K N V K E
----- T-3 -----
----- CB-14; CB-15; CB-16 -----
----- S-1 -----
110 120
S L K K P E T R N F T P E E F F S I F N R S I D A
--- T-1 --- T-4 (N109 nonglyco) ---
--- T-7 (N120 glyco); T-8 (N109 nonglyco) ---
----- CB-14; CB-15; CB-16 -----
----- S-5 or S-6 (N109 nonglyco) -----
130 140 150
F K D F M V A S D T S D C V L S S E L G P E K D S
----- T-5b -----
----- CB-6B -----
----- S-5 or S-6 -----
160
R V S V E K P F M L P P V A (A)
----- T-2 ----- (Carboxypeptidase)
----- CB-6B -----
----- S-2 -----

FIG. 12A

OLIGO	SEQUENCE	LOCATION
219-21	ACATTCTTIGGIGCATTTCTCCTCCAT G T G T T	393-368
219-22	AAAACTCCTCIGGIGTAAATTT G T T G G	447-425
219-25	GTTTCNGGTTTTT C C C	420-407
219-26	ATGGAAGAAACGCCCCCAAAACGT G G T G T	368-393
222-11	CCNAATGATTATATGATAAC C C C C T	167-186
222-12	GGNGGNAACATAAANGGCTT G G T	566-585
223-6	ACCATAAAATCTTTAAACGATC G G C G G	492-470
224-24	GTATTTTCAATAGATCCATTGA	450-471
224-25	CCAACTATGTCGCC	190-202
224-27	GTAGTCAAGCTGACTGATAAG	273-253

FIG. 12A cont.

224-28	TACCCAAACATGACTAGGCAA	235-215
225-31	TTCCAGAGTCAGTGTC	547-562
227-29	GCGAAGCTTGCCCTTTCCTTATGAAGAAGA	16-35 *
227-30	GCGCCGCGGTTACGGTGGTAACATGAAGGCTTTGTGA	586-561 *
228-30	GATAAATGCAAGTGATAATCC	45-65
230-25	GCGGTCGACCCCGCGGACTTTAAGTCCATGCACAC	705-685 *
237-19	CACCCGCGGTTATGCAACAGGGGGTAACATAATGG	569-592 *
237-20	CACCCGCGGTTAGGCTGCAACAGGGGGTAACATAAA	572-595 *

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACCTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190

FIG.12C

OLIGO	SEQUENCE
201-7	CCCCCCCCCGG T A
220-3	TTTTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCCCC
221-12	TTCGGCCGGATAGGCCTTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNNT
228-29	GGCCGGATAGGCCTCAC

FIG.13A

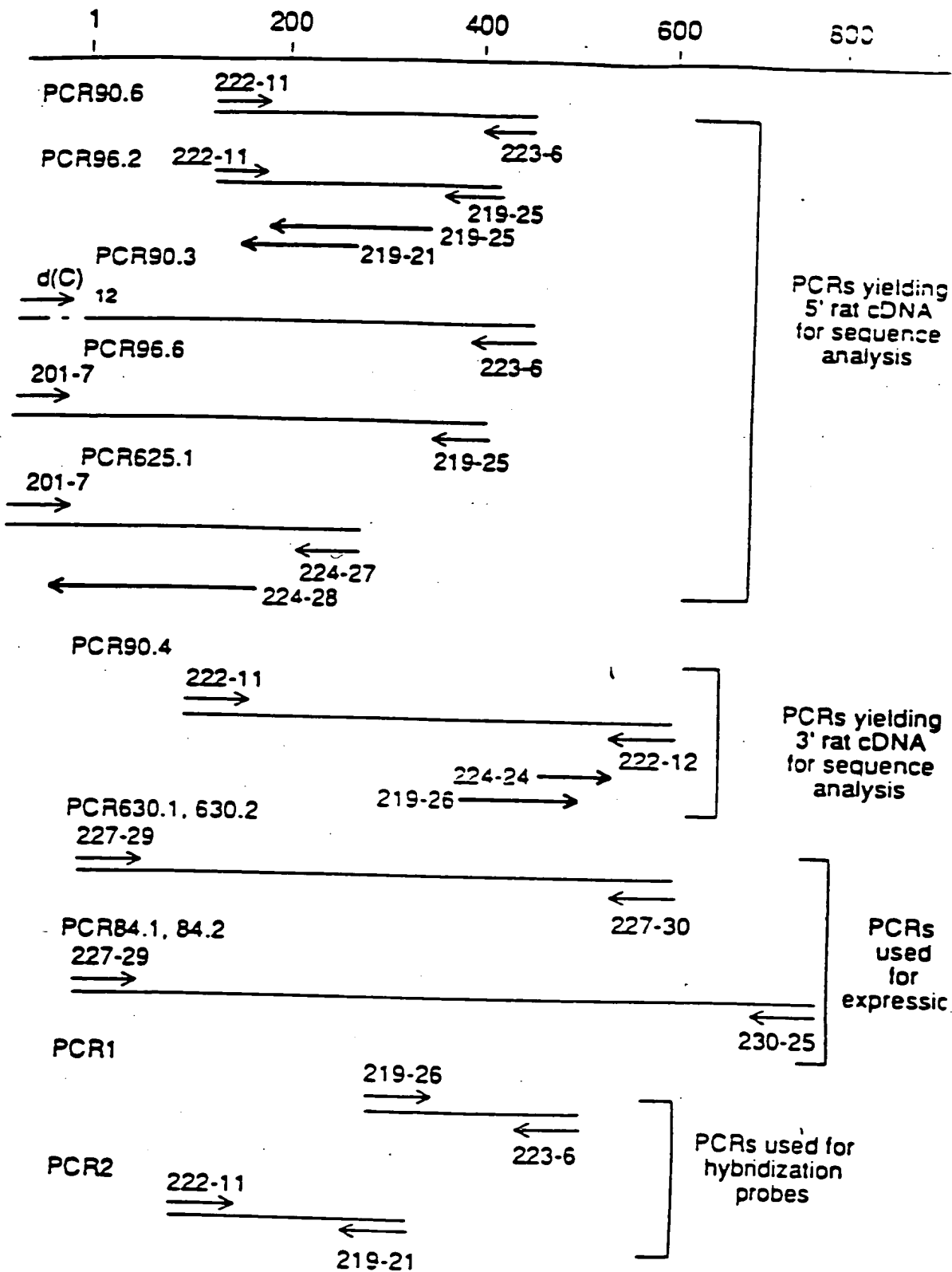


FIG. 13B

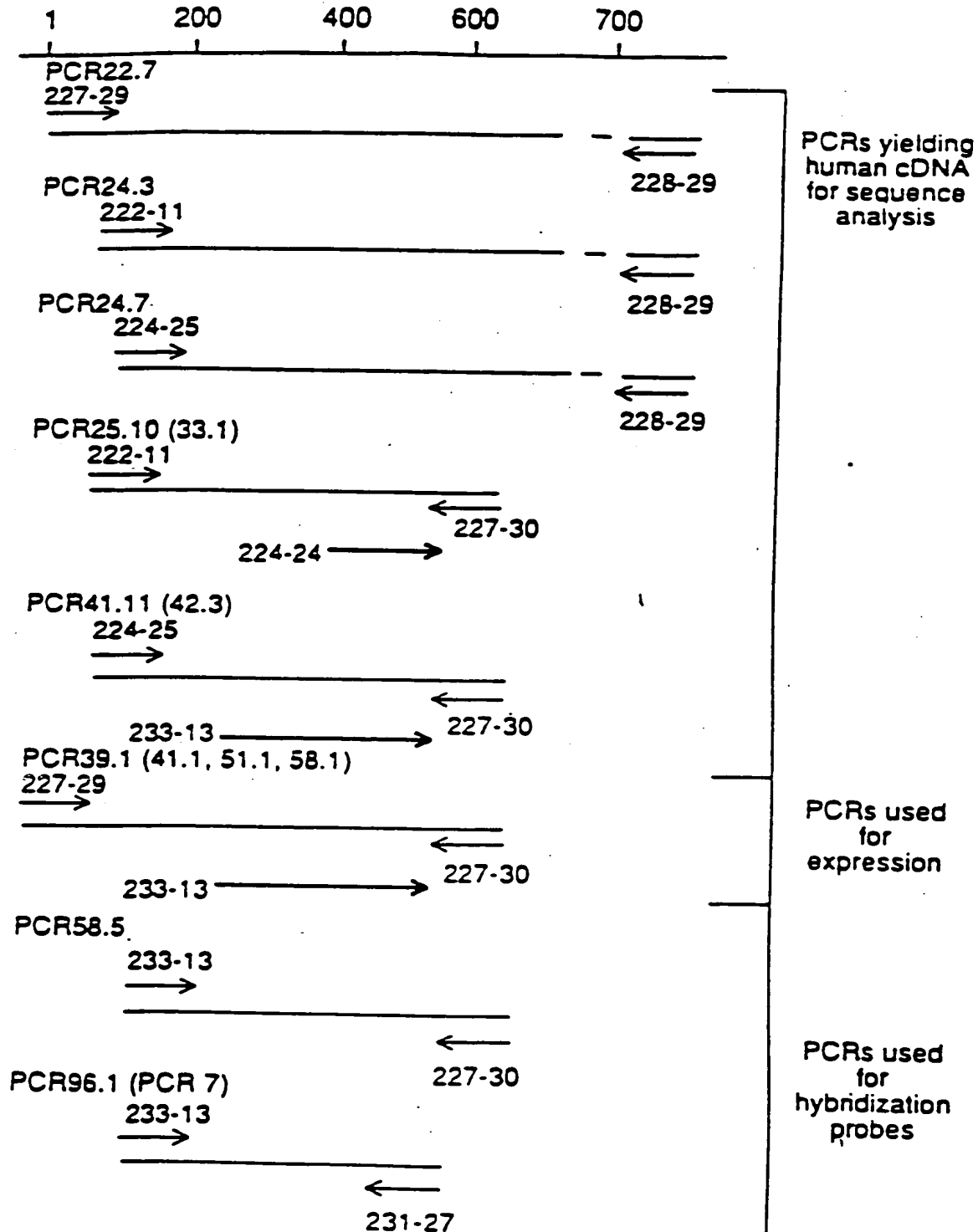


FIG. 14A

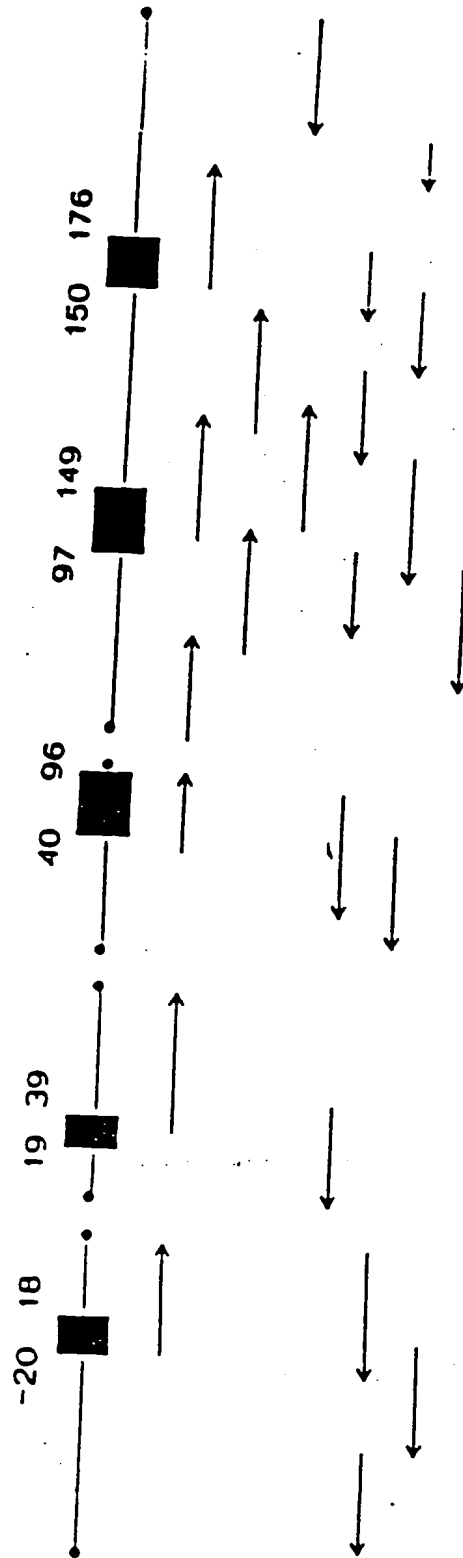


FIG. 14B

AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCATAAGTGGT 45
AAACAACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT 90
TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA 135
TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT 180
TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG 225
AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTTCATGCA TTCCT 270
CCATTTTCCGAGGTCCCCcCCcAAGTGATAATTCTGTTACACGTTG 315
CTACAAGTTCATCCCTAATTGCCGTCAAGAACTGACTGTAGAAG 360
GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT 405
AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC 450
TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT 495
AAGCCATCAGCTTAAAACAAAACAAAACAAAACAAAAAAACCC 540
CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC 585
TGGTTTGCATAGTTCTGGATTTTTTTTTTTTTTAAAACTGATGGAC 630
-20
ThrT-pIleIleThrC
ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT 675
-10
ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAACTC 720
1 10
lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA 765
18
hrLysLeu

FIG. 14B CONT.'

CAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC	810
CTGTGCTTGCTGACCACATAGGTTTCAGGGCACTCCCGACAGGAGT	855
TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC	900
TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC	945
TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT	990
TTGCCTGTTACCTACTG	1007

Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA	45
TTTACAACCTCAAGCATTATATATTGGACAACnACGGGGTATGAGA	90
TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT	135
	19
	Val
TCTCTTGTATTTACTCACGTTTTTCATTTCTTGGTCTCTGTAGGTG	180
	30
AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla	
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC	225
	39
GlyMetAspValLeu	
GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT	270
TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT	315
TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT	360
TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT	405
TAAGCCTACTCATTAAAAGGAAATGGCTCATCTTAGACGTAGCAA	450

FIG.14B CONT.'

CCGATGTTAATTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG	495
TTAAAATCATGTAAATTTCCCTCCTTGGCTATGTTATTTCTCATG	540
GCTATGTTATTCCTATTCGTATTTCAATTTAAAGGGACGGAATATT	585
TATTGTATTTCTGAACTTTTTCAGGCATGCATCCGGGTCTTTGAA	630
TAAAA	635

Intervening sequence of unknown length

CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA	45
ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA	90
GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGGTGGGGCAAG	135
AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG	180
GGTGGTTTAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT	225
TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT	270
TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAACTCTTTGTCTCT	315
GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA	360
ATCTGCCATATTTTAAATAGATGCTTTGTCTTCTCTTTGAATTTC	405

40.	50	
ProSerHisCysTrpLeuArgAspMetValThrHisLeu		
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA		450

60		
SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer		
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT		495

70	80	
GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle		

FIG.14B CONT.'

GAAGGCTTGAGTAATTATTCCATCATAGACAACTTGGGAAAATA 540

90 96
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA 585
ACTTGGTATTCATCAGAATTATTTTTCTTATACT 619

Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA 45
GAGGACATTATCCCCTCTTTGGATGCCATAGGAATCTGCTCTCAA 90
ATATGTAGATAACCACCTCTGCCACCTCAGCACATACATACACATA 135
ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC 180
TTTTCTGTATTTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT 225
TTAAAGGCTAATTCTTATTTTGTAATAAGCAGCTTTAAAATTCTT 270
AATTGTTTTTTTCGGGTCACCTTTATTGTCCTATTGCCACGACATTG 315
TCCTGTCCCATTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC 360
CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC 405
TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTTAAATT 450
ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC 495
AGTCAAGTCTATGAGTTATTTGAAAAGTCTAGTCTTTGTTAATTA 540

97
AsnValLys
TTTGTTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA 585

100 110
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu

FIG. 14B CONT.'

GAATCACTGAAGAAGCCAGAACTAGAACTTTACTCCTGAAGAA	630
120	
PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC	675
130	140
MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA	720
148	
GlyProGluLysA GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTCTTGTTTAAATGT	765
ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC	810
TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA	855
ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT	900
GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA	945
AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT	990
GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA	1035
AGATTTACGTCTCATGTCTTTTCCATAAGGTTCAAACCTCTGAGA	1080
CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC	1125
CCGAGCTGGGTCCCTATGGGGGAACTAACTTCATTGCTTTCTTTT	1170
AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT	1215
TCCTAAGCATGTCTGTGCATGCaATAAGCCTTCACTCTACAAGAC	1260
AGTTATGGTGTATCGCTTGACAAAACCTGAGCAGCCAAGCTGAGTA	1305
TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT	1350
GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAGTTCA	1395

FIG.14B CONT.

	150	
	spSerArgV	
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG		1440
	160	
alSerValThrLysProPheMetLeuProProValAlaAlaSerS		
TCAGTGTCAAAAACCATTTATGTTACCCCCTGtGCAGCCAGTT		1485
170	176	
erLeuArgAsnAspSerSerSerSerAsn		
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC		1530
TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT		1575
GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG		1620
TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG		1665
TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA		1710
ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTTAAATAAGGCAC		1755
GAAATTAATTGAAGGAAAAAAAAAATACAAGCAAGGCCTTATTTTG		1800
AATCATGGTAGGCTTAAAATAGACTTTGTGGAGAATGTCCCTGAT		1845
CAAAGTGGAGTTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC		1890
AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG		1935
CATGTTTGGAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA		1980
TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT		2025
TGcCCAAGAACCCAcGTTCCCTGGAAGACTATCTTATTTTCATGTC		2070
TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT		2115
CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA		2160
AAGAAAGTTCTCTGAAGTCCATGCTTTAGAATGTTTCTCTATCAA		2205

FIG. 14B CONT.'

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC	2250
CCTGAAAAATATATTTACAGTG TAGACATTTGATATACATCTAA	2295
GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC	2340
CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC	2385
ATGCATATAACATATCAGATCCTCGAGC	2413

CTGGATCGCAGCGCTGCCTTTCCCTTATGAAGAGACACAACCTTGGATTATCACTTGCAT	60
-25	
M K K T Q T W I I T C I	-20
Y L Q L L L F N P L V K T Q E I C R N P	1
TTATCTTCAACTGCTCCTATTTAATCCTCTCTGTCANAACCTCAGGAGATCTGCAGGAATCC	120
-10	
V T D N V K D I T K L V A N L P N D Y M	20
TGTGACTGATAATGTAAAGACATTACANAACCTGGTGGGAATCTTCCAAATGACTATAT	180
-30	
I T L N Y V A G M D V L P S H C W L R D	40
GATAACCTCAACTATGTGCGCGGATGGATGTTTGCCTAGTCATTGTTGGTTACGAGA	240
-50	
M V T H L S V S L T T L L D K F S N I S	60
TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAAATATTTTC	300
-70	
E G L S N Y S I I D K L G K I V D D L V	80
TGAAGGCTTGAGTAATTATTCCATCATAGACANAACCTTGGGAAATAGTGGATGACCTCGT	360
-90	
A C M E E N A P K N V K E S L K K P E T	100
GGCATGTATGGAAGAAATGCACCTAAGAATGTAAAAGAATCACTGAAGAAGCCAGAAAC	420
-110	
R N F T P E E F F S I F N R S I D A F K	120
TAGAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAA	480

FIG.14C CONT.

130
D F H V A S D T S D C V L S S T L G P E
GGACTTCATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTAGGTCCTGA 540

150
K D S R V S V T K P F M L P P V A A S S
GAAAGATCCAGAGTCAGTGTCAAAACCATTATGTTACCCCTGTTCAGCCAGTTC 600

170
L R N D S S S S N R K A A K S P E D P G
CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAGCCGCAAGTCCCTGAAGACCCAGG 660

190
L Q W T A M A L P A L I S L V I G F A F
CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTGCTTGTAAATGGCTTTGCTTT 720

210
G A L Y W K K K Q S S L T R A V E N I Q
TGGAGCCTTATAC TGGAGAAGAAACAGTCAGTCTTACAAAGGCGCAGTTGAAATATACA 780

230
I N E E D N E I S M L Q Q K E R E F Q E
GATTAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGATTCAAGA 840

248
V
GGTGTAAAT 849

FIG.15A

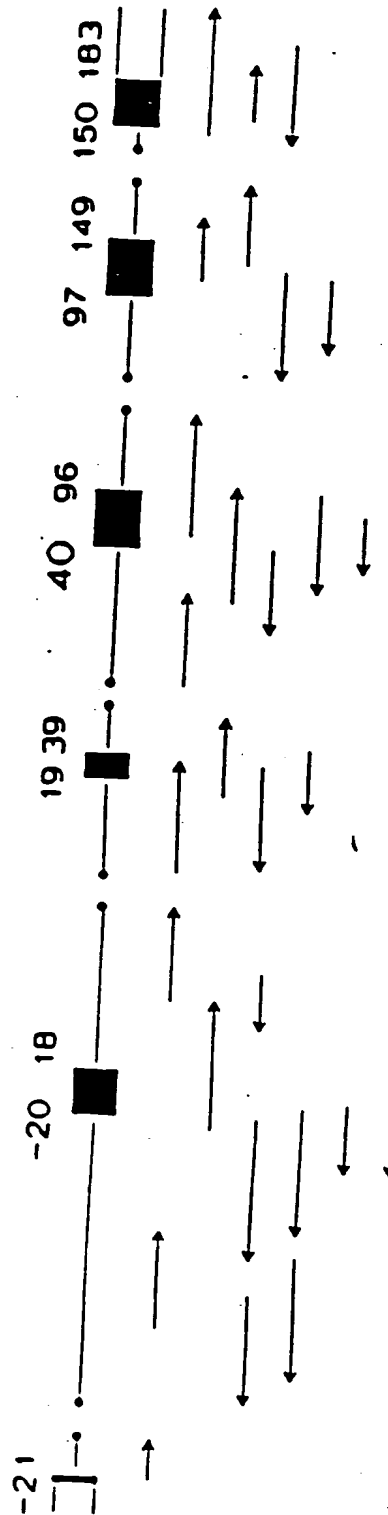


FIG.15B

-21
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA	45
AAAATCGCGCCCGGTGCCCCGGGGaAGCCGGCGCTCCCTGGGACT	90
TGCAGCTGGGGCGTGcAGGGCTGTGCCTGCCGGGTG	126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA	45
CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT	90
ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG	135
TGTTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT	180
TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG	225
GCTAAAAAGCTGTGTTTCAAAATATTCTTTTGATGTCTCACAAAT	270
TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT	315
TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA	360
GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA	405
ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT	450
CTCTAGTTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC	495
TGCTACAAGTTTATTCTTAATTGCCATTGGGAAATTGGCTGAAGA	540
AAGTTTTTAAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT	585
CAAAATGGATTTTAACTAAAAGCTTTTAAAAACTTTGGTGAGCAT	630
AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT	675

FIG.15B CONT.'

ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT	720
TTGAATGATTACAGATCTTAAGTATGATCACCAGCAATTTTTC	765
<div style="display: flex; justify-content: space-between; width: 100%;"> -20 -10 </div> ThrT=IleLeuThr=CysIleTyr=LeuGlnLe	
TGTTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT	810
<div style="text-align: center;">1</div> uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs	
GCTCCTATTTAATCCTCTCGTCAAACTGAAGGGATCTGCAGGAA	855
<div style="display: flex; justify-content: space-between; width: 100%;"> 10 18 </div> nArgValThrAsnAsnValLysAspValThrLysLeu	
TCTGTGACTAATAATGTAAAGACGTCCTAAATTGGTAAGTAA	900
GGAATGCTTTACCGTGCTGTGTAAAAAGAGCTGTGGCTCTTTTT	945
CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT	990
AATGTTTTCTTAAAGTGGGGAAAGTAATCACTGGGTTACAATAAA	1035
GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA	1080
TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT	1125
TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT	1170
TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC	1215
CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA	1260
CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT	1305
GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC	1350
ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT	1395
CATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTACAT	1440
TGAACTCTTCCCTCAGCGAAAGCATTTCGATTGCTTCCC	1479

FIG.15B CONT.'

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC	45
CAAACCTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA	90
GTCTAAAAGATCTGTATTATCACTTTTTTTATTTTGAAGGATGCCT	135
TTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT	180
AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAAACAGTTTTG	225
TGTGCTTTTCTCCAAAGCACTACAAATATGATTAAATTGATGTATA	270
	19
	ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTTTGTCTCTGTAGGTGGCAA	315
	30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM	
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA	360
	39
etAspValLeu	
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGT	405
AGCTCATAGAAGAAATGGGATCATTATATTGAGATAGTACACTA	450
GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA	495
TCTTTGGAATTTGACTTGCAGGCTTTTTTTTTCCCCCTCTT	535

Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTAGAATAGTCCCTCCTCCT	45
CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC	90

FIG.15B CONT.'

CTCCTATTACAACATTTTAAAGTAATGTAATATTAATTTTAAAAAT	135
CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG	180
AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAG	225
CCTGGCCAACATGGTGAACTTCCTCTCTACTAAAAATAAAAAAG	270
TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA	315
GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG	360
AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT	405
40	
ProSerHisCysTrpIleS	
TTTGTCTCTTTTTTTCATATCTTGACGCCAAGTCATTGTTGGATAA	450
50	
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA	60
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG	495
70	
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI	
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA	540
80	
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL	90
TAGACAAACTTGTTGAATATAGTGGATGACCTTGTGGAGTGCGTGA	585
96	
ysGluAsnSerSerLys	
AAGAAAACCTCATCTAAGGTAACCTTGTGTTTCATTGGGATTATTTT	630
TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG	675
AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC	720
AAATTTAAAAATCTTGTTTCAGATGAGCAAAGAAAACAAGTATTTG	765
CAGTTATACTGCAATACTGAAGTGACATTC	796

FIG.15B CONT.'

Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA	45
CTACCCTGCATTACCAATCTGAATTACATACGTTAAACAGCCAT	90
CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA	135
GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA	180
97	
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAA	225
110	
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT	270
120	
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV TCTTTAGAATTTTAAATAGATCCATTGATGCCTTCAAGGACTTTG	315
140	
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS TAGTGGCATCTGAACTAGTGATTGTGTGGTTTCTTCAACATTAA	360
148	
erProGluLysA GTCCTGAGAAAGGTAAGACATGTAAGCATTTCAGTTCAAATGTA	405
AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG	450
TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG	495
CAGATATCAATAGCACAGAAGAAA	519

Intervening sequence of unknown length

FIG.15B CONT.'

CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG	45
150	160
spSerArgValSerValThrLysProPheMetL	
CTTTCTATTTAGATTCCAGAGTCAGTGTACAAAACCATTTATGT	90
170	
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS	
TACCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA	135
176	
erAsnA	
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA	180
ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAACTTCT	225
ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA	270
TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG	315
CTGGAGATAATGTTTGTAGAGAATTAGGCCAATAAATTT	352

FIG.15C

-25
 M K K T Q T W I L T C I Y L Q
 AAGCTTGCCTTTCCTTATGAAGACACAAACTTGGATTCTCACTTGCATTATCTTCAG 61
 -10
 L L L F N P L V K T E G I C R N R V T N
 CTGCTCCTATTAACTCCTCTCGTCNAAACTGAAGGGATCTGCAGGAATCGTGTGACTAAT 121
 1
 N V K D V T K L V A N L P K D Y M I T L
 AATGTAAAGACGTCACCTAATTTGGTGGCAATCTTCCAAAGACTACATGTAACCCCTC 181
 20
 K Y V P G M D V L P S H C W I S E M V V
 AAATATGTCCCCGGGATGGATGTTTGGCCAAAGTCATTGTTGGATAAGCGAGATGGTAGTA 241
 40
 Q L S D S L T D L L L D K F S N I S E G L
 CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTCAATAATTTCTGAAGGCTTG 301
 60
 S N Y S I I D K L V N I V D D L V E C V
 AGTAATTATCCCATCATAGACAAACTTGTGTAATATAGTGATGACCTTGTGGAGTGCCTG 361
 80
 K E N S S K D L K K S F K S P E P R L F
 AAAGAAACTCATCTAAGGATCTAAAAAATCATTCAGAGCCCCAGAACCCAGGCTCTTT 421
 100
 110

FIG.15C CONT.

T P E E F F R I F N R S I D A F K D F V 120 130
ACTCCTGAAGAATCTTTAGAAATTTTAATAGATCCATTGATGCCCTTCAAGGACTTTGTA 401

V A S E T S D C V V S S T L S P E K D S 140 150
GTGGCATCTGAAACTAGTGAATGTGTGGTTCTTCAACATTAAGTCCTGAGAAAGATTCC 541

R V S V T K P F M L P P V A A S S L R N 160 170
AGAGTCAGTGTCACAAAACCATTATATGTACCCCTGTTCAGCCAGCTCCCTTAGGAAT 601

D S S S N S K Y I Y L I 180 183
GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCAAT 661

TAGCACCTATAGGAGTATTCATGGGCTTCAAGGAAACTTCTACATTTATTATTATGA 721

TACTGTTCTGTACTGTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTGTAGAAATTA 781

AATTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG 820

FIG. 15D

GAGCTCCGAGCCCTCTCTGGCGCGAGGTATTTCTGTCTGTnCCCCGGGGTGCCAGGTGA 60
GCCCCAGCGGATCCGGGAGGGTAACTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC 120
AAGCTTCGCCCTCTGCGTCCCCCGGCCCTTCGCGGTCTCCCGCCAGTGCAGGTCCGGGGCC 180
CCCAGGGGAGCGGACAAGGTTGGCCTAACTCTGCCMAACTTCTGGGCATTTACCGTGCTC 240
TGGCGGCCCTCCCGATTCTTCCCCTCGCGGCCCTTGCCCTGCTTCTCGCCTACCCCGGGCTC 300
CGGAAGGGNAGGAGGCGTGTCCGGAGCAGCGCGGGGGACTGTATAAAGCGCGCGCGG 360
CTCAGCAGCCGGCTTCGCTCGCCGCCCTCGGCGCGAGACTAGMAGCGCTGCGGGNAGCAGG 420
GACAGTGGAGAGCGCGCTGCGCTCGGGCTACCCCAATGCGTGGACTATCTGCGCGCGCTGT 480
TCGTGCATATTTGGAGCTCCAGMACAGCTAAACGGAGTCGCCACACCACTGTTTGTCG 540

-25 -21
Met Lys Lys Thr Gln
TCGATCGCTATTTGCTTTCCTTATGMAAGACACACAGTAGTAGGGCGCGCCCGGA 600
GC'CCCCAGGCTCTCCAGGAAATACTCGGCCCGGTGCCCGGGMAGCCGGCGCTCCCTGG 660
GACTTGACAGCTGCGGGGTGCAGGGCTGTGCCTGCCGGGTGAGACAAGAGGATGCGGGGA 720
GGCCGGCGTGGTGTGTGATCCCGAGCGGAGCCGnnTGAGCCAGGGAGAAAGAGTGGA 780
GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCTCAGCAGTTAAGTTTGTAGCTGTCAG 840
TCGGAACCGTAATTCCCGTCTGTGTGGAAGATTGGCTTTTnGCCACCGGAATGTAAATT 900
ATCAC

AGATACTACAAAGATMAATCAGTTGCACAAAGTTCTTGAACTCTACAGTGTAAATAAGGMA	60
AAATAAGTCATGCATAAAAGCAACTATAATACATMAATAGAAATGTTATTTTCMAAGCCGA	120
TGTGTAGGTTATGTGTGTCGAGAGAGAGAGAGAGACAGATTACTTTCTGCTAGGGT	180
TCAAGNATGCCTTCCGTGGCTAAGGMAATATTTTCCTTAAGTGGCTAANMAGCTGTGT	240
TTCMAAATATTTCTTTTGATGTCTCACMAATTCAGTGGMAATCTCTTAGGTCTMAAATAAT	300
ACATCTCTCTCACTTTAACTTGGTGTGCTATTGTAGATTATTGGATTMAAGCACTGCTCA	360
GGGATTATGCTTGCTTCTTGCCCAAGCAGCTCTACATTTNMGTAGMAATAGATGTTTCTTT	420
TGGTGCCCATNAGGTATACATTTTATGCATTCTCTAGTTTTTAGMAGATACCCCTAAGGGCT	480
NAGTCTTTAACAATGCTGCTACAAAGTTTATTTCCTMAATGGCCATTGGGMAATTTGGCTGNAGA	540
NAGTTTTTAATAAAGTTAACMAATATTGTCATTGAGAGAAATMAATTCMAAATGGATTTTAA	600
CTMAAGCTTTTAAAAACTTTTGGTGAGCATAGCTTGAAATGCGTAATATTTAATTGCATTT	660
NAGCCNATMACATATATTAGACTGGTCTTTTGTGTCATCAAGGCATTAGATGTTAAAGT	720
-20	
Th	
TTGAATGATTACAGATCTTAACTGATGATCACCAGCAATTTTCTGTTTTTCATTTTAGAC	780
-10	
RTpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrGI	
TTGGATTCTCACTTGCATTTATCTTCAGCTGCTCCTATTTAATCCTCTCGTCAAACTGA	840

FIG. 15D CONT.

1	10	18
uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu		
AGGGATCTGCAGGMAATCGTGTGACTAATATGTANAAGACGTCACATAATTGGTAAAGTAA	900	
GGMATGCTTTACCGTGTGTGTANAAGAGCTGTGGCTCTTTTTCCTGTGCTTGTGAT	960	
AAAAGATTAGATTTTCTTGCCCCCAAGTAAATGTTTTCCTAAGTGGGMAAGTAATCA	1020	
CTGGGTTACAATAAAGGTTTATAGMAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA	1080	
TTTGTGGTNMAACTGGCTAGTTGCACACCACTGCTGTGACTGCTTCTTTGCTGCTCTTC	1140	
TCCCCATCCTTCATAGGCAGTGAAGGACCTTGGAGAGTTCGCTGTGTGCTGATGGGCTTG	1200	
CCCCAGCTTGTTCCTCCCATATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTTCCCTTCA	1260	
CATGCTCTTCTACTCTTCTTTANAAAGCCTAACGNMAGGMAATCTGMAATGGCTATTCTC	1320	
CCNATTCAATTAAGCAGGMAAGACCCTGTGCACATGTCACTGGGTGTTTGCTCCTTCAGGGAA	1380	
CATAGAGAGCTTATTCATTGGCCACATGTTGMAGGGACTCATCTCCCTGGTTGTGCACAT	1440	
TGAACCTCTTCCCTCAGCGMAAGCATTTGCATTGCTTCCCT	1479	
Intervening sequence of unknown length		
GAATTCCAAGATCACAGGTGGAAGGTGAAATTCAGATCATGTTCCAAACTCAGTAGGT	60	
TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAGATCTGTATTATACACTTTTTTA	120	
TTTTGAAGGATGCCCTTTTGATTACAGAGGGGAAATCAAGGATTAAAAATCAATATACATGT	180	

FIG. 15D CONT.

AAATATTGAAATTCATTGGTAACTTTAAAGACACACAGTTTGTGTGCTTTTCTCCMA	240
AGCACTACAAATATGATTAATTGATGTATMGMATTTTCTTATGGMAATTTTTTTTTGT	300
19	
ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM	
30	
CTCTGTAGGTGGCAATCTTCCAAAGACTACATGATAACCCCTCAATATGTCCCCGGGA	360
39	
etAspValLeu	
TGGATGTTTTTGGTATGTMAACTACATTTCTGAGTTTTCATTTTAGTAGCTCATAAGAAA	420
TGGGATCATTCATATTGAGATAGTACACTAGCTGCTATTTAGGAGCTTGCTTATTGTCAG	480
GATTTGAGAAATTTATCTTTGGMAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT	535
Intervening sequence of unknown length	
CCTGTTACAAATATCCCTCCTCTATTACANTAGTCCCTCCTCCTGTACACTAGTC	60
CCTTCTCTTCTTTTACAAATMACCCCTGCTCCTCTATTACAACATTTTAAAGTAATGTAAT	120
ATTAAATTTTAAAAATCTGGCCAGGCACGGTGGTTTCATGCTTGTAAATCCAGCACATTGGG	180
AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCCAACATGGT	240
GAAACTTCCTCTCTACTAAAAAATAAAAGTAGCCAGGCATGGTGGCAGGCACCTTGTAAT	300
CTGAGCTACTCGAGAGGCTGAGGCAGGAGAAATCACTTGAGTAACATAAACGATAGCTTTG	360
AAGAGTACTCCGAGTTTTTATGGCACTTACTTATTAAATAAGCTGTTTGTCTCTTTTTTC	420

FIG. 15D CONT.

40	ProSerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerL	50	
	ATATCTTGCAGCCNAGTCATTGTTGGATNAGCGAGATGGTAGTACAAATTGTCAGACAGCT	400	
60	euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI	70	
	TGACTGATCTTCTGGACAAAGTTTTCAAATATTTCTGMAGGCTTGAGTAATTTATCCATCA	540	
80	IeAspLysLeuValAsnIleValAspLeuValGluCysValLysGluAsnSerSerL	90	
	TAGACMAACTTGTGATATATAGTGGATGACCTTGTGGAGTGGTGAAAGNMACTCATCTA	600	
96	ys		
	AGGTAACTTTGTGTTTCATTGGGATTATTTTTCATTACGCTTCTTAAMACCCTGCTTC	660	
	TTGGTGCTGTTGGGGMAATGAGGCACCTTTATTTATGATATTTTGTGATATAACTTC	720	
	AAATTTMAAANAATCTTGTTTCAGATGAGCMAAGMAACMAGTATTTTGCAGTTATCTGCMAAT	700	
	ACTGMAGTGACACATTC	796	
	Intervening sequence of unknown length		
	TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACCTGGGATCACTACCCCTGCATTACC	60	
	AATCTGAATTACATACGTTAAACAGCCCATCTAAAGTGCTAGTTGTAAGAGTCTAATA	120	
	CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCTCAGTTMAGTCTGAAGA	180	
	97		
	AspLeuLysLysSerPheLysSerP		
	CTATTTGAAAATGTAAATCCCTATTTTTTCTTCTAGGATCTAAANAATCATTCAGAGCC	240	

FIG. 15D CONT.

```

110      roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspA
120      CAGAACCCAGGCTCTTTACTCTCTGAAGAATTCTTTAGAAATTTTAAATAGATCCATTGATG
300
130      laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS
140      CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTTCCTTCACATTTAA
360
148      erProGluLysA
150      GTCTGAGAAAGGTAGACATGTAGCATTTCCAGTTCAATGTAAACMACAACTTAA
420
160      TCTTCCCTNTGTAGTAAGNATCTACCTCTGTGTGTAGCTGTAGCMAGATACATGCATGTA
400
170      CGTCTAATAAAMAGCAGATATCAATAGCACAGMAGMMACTAATGATTGTAGATTGTGGG
541
Intervening sequence of unknown length
spS
150      CTCTATATATGCTATACAAATCACCATATATACACTGACACATTATTGCTTTCTATTAGATT
60
160      erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA
170      CCAGAGTCAGTGTGCACAAACCATTTATGTATACCCCTGTGTGCAGCCAGCTCCCTTAGGA
120
176      snAspSerSerSerSerAsnA
180      ATGACAGCAGTAGCAGTAATAGTAGTAAAGTACATATATCTGATTAAATGCATGCATGGCTCCA
180
240      ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAACCTTCTACATTTATTATTATT
240
300      GATACTGTTCTGTACTGTTATTCCCTTTTATGGTCTTCTTGGAGACTTAAGTTTGTAGAAT
300
```

FIG. 15D CONT.

TAAATTTCCCTAGAGCTGGAGATATGTTTAGAGMATTAGGCCAATAAATTTCTGCTGA	360
GGTTATTTTAAATAAGACATAAAATTTAATTTTAGAATATGATTTATGCCTTTTGTGMA	420
TCATTAACATATAT	434
Intervening sequence of unknown length	
ACAGAAACAGTTTAAACAACACACAGCATAGAGGAAACTTCTAGMATGGATATGCTGTA	60
178	
TTCATCAGTGTGTTCTTTAATTTATAGGGNAGGCCAATAATCCCCCTGGAGACTCCAGCC	120
190	
euHisTrpAlaAlaMetAlaLeuProAlaLeuPheSerLeuIleGlyPheAlaPheG	200
TACACTGGGCACACCATGGCATTGCCAGCATTTGTTTCTCTTATAATTGGCTTTGCTTTTG	180
213	
lyAlaLeuTyctTrpLys	
GAGCCTTATACCTGGMAGGTAAAGTGGTACCATTCCCTTTTNNMAATATGCTATGTTTAC	240
ATAAATTATCATCTTTTTTTCCTCAAGMATGATCCTTAAAGMAACAGTGAATCTACCT	300
TAGCTTATACTAAACAAATTTAAATTTTATAAAGTTTCCTGTTTCTCATTATGCTGGA	360
GACATCCCTCTAGCTGATAATTCAGGCTTAAGAATTAGGAACT	404
Intervening sequence of unknown length	

AAACTGTTATTGGAGTTATTGCCATMAAGATAAAMGTGGAGTCCACTTACCTCTTAAA	60
TATTAGACCATTCAATTGATTATTTTACAGTATATGTCTTTCTTCTTTTTCCAGAAGAGAC	120
InProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIles	180
AGCCAAGTCTTACAAGGGCAGTTGAATATATACAAATTAATGAAGAGGATMATGAGATMA	240
GGTATTTTGTTTTGCTAAATGTGTGCCCATCMGCNTGACATTGCCATTTTCACACACTG	300
TGTACCTGCCCATAAATGTCTTTMAGMAGTCCTTCACTCATGACAGTAGCTCCTAACCCAGT	344
GAGTCCCCMACTCTATCCCATGTTTCTGTATGTCTCACCTCTCTCTTC	
Intervening sequence of unknown length	
GTATGTGTATATATATATACAGAGAAAGAAATGTTTAACTACTTGGAAAGACTACCTTA	60
AGACAAATGAACTCTTCCCCTCTTCCCCTATATAGTAAATAAGAAGGTAGGCTCCCCCATTCAAAT	120
TTTGCAATCTTCTGCTACTATATTTACAGAAAGCTGCCATTTTACAAATGCCGAGATCATG	180
GTGTACCTCAGAATCTCTGACCAAGAGCAAATAAGCATTTtTTCTTATTGTTTTTTCAGTA	240
etLeuGlnGluLysGluArgGluPheGlnGluVal	300
TGTTGCAAGAGaaAGAGAGAGAGTTCACAAAGTGTAAATTGTGGCTTGTATCAACACTGT	360
TACTTTCGTACATTGGTAAGTTTTTTTTTCTCTCTTCCCTTTTTTTTCTTTTTTTTATTATA	

FIG. 15D CONT.

CTTTAAGTTCTAGGTACATGTGCACAMTGTGCAGGTTTGTTACGTATGTTTACATGTGC 420
CATGTT 426

FIG.16A

	Human	Monkey	Dog	Cat	Cow	Rat	Mouse	Chicken	Scfpop
25	MRKKTQTWILT	CYYLQLLLEN	PLVKTEGICR	NRVTNNVRKDV	TKLVANLPKD				
	MRKKTQTWILT	CYYLQLLLEN	PLVKTEGICR	NRVTNNVRKDV	TKLVANLPKD				
	MRKKTQTWIIIT	CYYLQLLLEN	PLVKTKGICG	KRVTDVVKDV	TKLVANLPKD				
	MRKXTQTWIVT	CYYLQXLLFN	PLVKTKGLCR	NRVTDDVVKDV	TKLVANLPKD				
	MRKKTQTWIIIT	CYYLQLLLEN	PLVHTQGICS	NRVTDDVVKDV	TKLVANLPKD				
	MRKKTQTWIIIT	CYYLQLLLEN	PLVKTQEICR	NPVTDNVKDI	TKLVANLPKD				
	MRKKTQTWIIIT	CYYLQLLLEN	PLVKTKREICG	NPVTDNVKDI	TKLVANLPND				
	TWIIIT	CFCCLQLLLLN	PLVKAQSSCG	NPVTDDVNDI	TKLVANLPND				
	MRKKTQTWIIIT	CYYLQLLLEN	PLVkt.gicr	nrVTd.vkdv	TKLVANLPKD				

	Human	YMITLKYVPG	MDVLPShCWI	SEMvVQLSDS	LTDLldKFSN	ISEG...LSN	72
Monkey	YMITLKYVPG	MDVLPShCWI	SEMvVQLSDS	LTDLldKFSN	ISEG...LSN		
Dog	YKIALKRYVPG	MDVLPShCWI	SVmVEQLSVS	LTDLldKFSN	ISEG...LSN		
Cat	YKIALKRYVPG	MDVLPShCWI	SVmVEQLSVS	LTDLldKFSN	ISEG...LSN		
Cow	YMITLKYVPG	MDVLPShCWI	SEMvEQLSVS	LTDLldKFSN	ISEG...LSN		
Rat	YMITLNYVAG	MDVLPShCWL	RDmVTILSVS	LTDLldKFSN	ISEG...LSN		
Mouse	YMITLNYVAG	MDVLPShCWL	RDmVIQLSLs	LTTLldKFSN	ISEG...LSN		
Chicken	YLITLKYVPK	MDSLPNHICWL	HLmVPEFSRS	LTTLldKFSN	ISEG...LSN		
Scfpep	Ymit:LkYVpg	MDvLPaHICwi	semVEqlSVs	LHNLlQKFSd	ISEG...LSN		
				LtdLldKFSn	ISEG...LSN		

	73		121
Human	YSIIDKLVNI	VDDLVECVKE	NSSKD. LKKS
Monkey	YSIIDKLVNI	VDDLVECVKE	-NSSKD. LKKS
Dog	YSIIDKLVKI	VDDLVECTEG	YSFEN. VKKA
Cat	YSIIDKLVKI	VDDLVECVEG	HSSSEN. VKK3
Cow	YCIIDKLVKI	VDDLVECMEX	HSSSEN. VKK3
Rat	YSIIDKLGRI	VDDLVACMEE	NAPKN. VKES
Mouse	YSIIDKLGRI	VDDLVLCMEE	NAPKN. IKES
Chicken	YSIINNLTRI	INDLMACLAF	DNKDFEIKEN
Scfpep	YsIIDkLvki	vdDLvEc.ee	nsakn.vKks

FIG.16B

122	Human	SIDAFKDF.V	VASETSDCVV	SSTL.SPEKD	SRVSVTKPEM	LPPVAASSLR	169
	Monkey	SIDAFKDF.A	VASETSDCVV	SSTL.SPEKD	SRVSVTKPEM	LPPVAASSLR	
	Dog	SIDAFKDF.LET	VASKSSECW	SSTL.SPDKD	SRVSVTKPEM	LPPVAASSLR	
	Cat	SIDAFKDF.LEM	VASKTSECW	SSTL.SPEKD	SRVSVTKPEM	LPPVAASSLR	
	Cow	SIDAFKDF.LEI	VASKMSECVI	SSTL.SPEKD	SRVSVTKPEM	LPPVAASSLR	
	Rat	SIDAFKDF.M	VASDTSDCVL	SSTL.GPEKD	SRVSVTKPEM	LPPVAASSLR	
	Mouse	SIDAFKDF.M	VASDTSDCVL	SSTL.GPEKD	SRVSVTKPEM	LPPVAASSLR	
	Chicken	TIEVYKEFAD	SLDK.NDCIH	PSTVETPEND	SRVAVTKTIS	FPPVAASSLR	
	Scfpep	oIdafKdf.m	vaektodCvv	oStl.oPeKd	SRVøVTKPfm	LPPVAASSLR	
170	Human	NDSSSSNRKA	KNPPGD	...SSLIWAAM	ALPAFFSLII	GEAFGALYWK	213
	Monkey	NDSSSSNRKA	KNPTGD	...SSLIWAAM	ALPAFFSLII	GEAFGALYWK	
	Dog	NDSSSSNRKA	SNSIGD	...SNLQWAAM	ALPAFFSLVI	GEAFGALYWK	
	Cat	NDSSSSNRKX	TNPIED	...SSIQWAVH	ALPACFSLVI	GEAFGAFYWK	
	Cow	NDSSSSNRKA	SNSIED	...SGLQWAAV	ALPAFFSLVI	GEAFGAFYWK	
	Rat	NDSSSSNRKA	AKSPED	...PGLQWTAM	ALPALISLVI	GEAFGALYWK	
	Mouse	NDSSSSNRKA	AKAPED	...SGLQWTAM	ALPALISLVI	GEAFGALYWK	
	Chicken	NDSIGSNTSS	NSNKEALGFI	SSSGLQGISI	ALTSLLSLLI	GFILGAIYWK	
	Scfpep	NDsøssNrka	.n..ed....	..øølqwaam	AlpalfSLVI	GFafGALYWK	
214	Human	KRQPSLTRAV	ENIQIN	...E	EDNEISMLQE	KEREFQEV	248
	Monkey	KRQPSLTRAV	ENIQIN	...E	EDNEISMLQE	KEREFQEV	
	Dog	KRQPNLRTV	ENIQIN	...E	EDNEISMLQE	KEREFQEV	
	Cat	KRQPNLRTV	ENIQIN	...E	EDNEISMLQE	KEREFQEV	
	Cow	KRQPNLRTV	ENRQIN	...E	EDNEISMLQE	KEREFQEV	
	Rat	KRQSSLTRAV	ENIQIN	...E	EDNEISMLQO	KEREFQEV	
	Mouse	KRQSSLTRAV	ENIQIN	...E	EDNEISMLQO	KEREFQEV	
	Chicken	KTHPKSRPES	NETIQCHGCQ	EENEISMLQO	KEREHLQV		
	Scfpep	Kkqpøltrav	eniqin	...ø	edNEISMLQø	KøørefQøø	

FIG. 16C

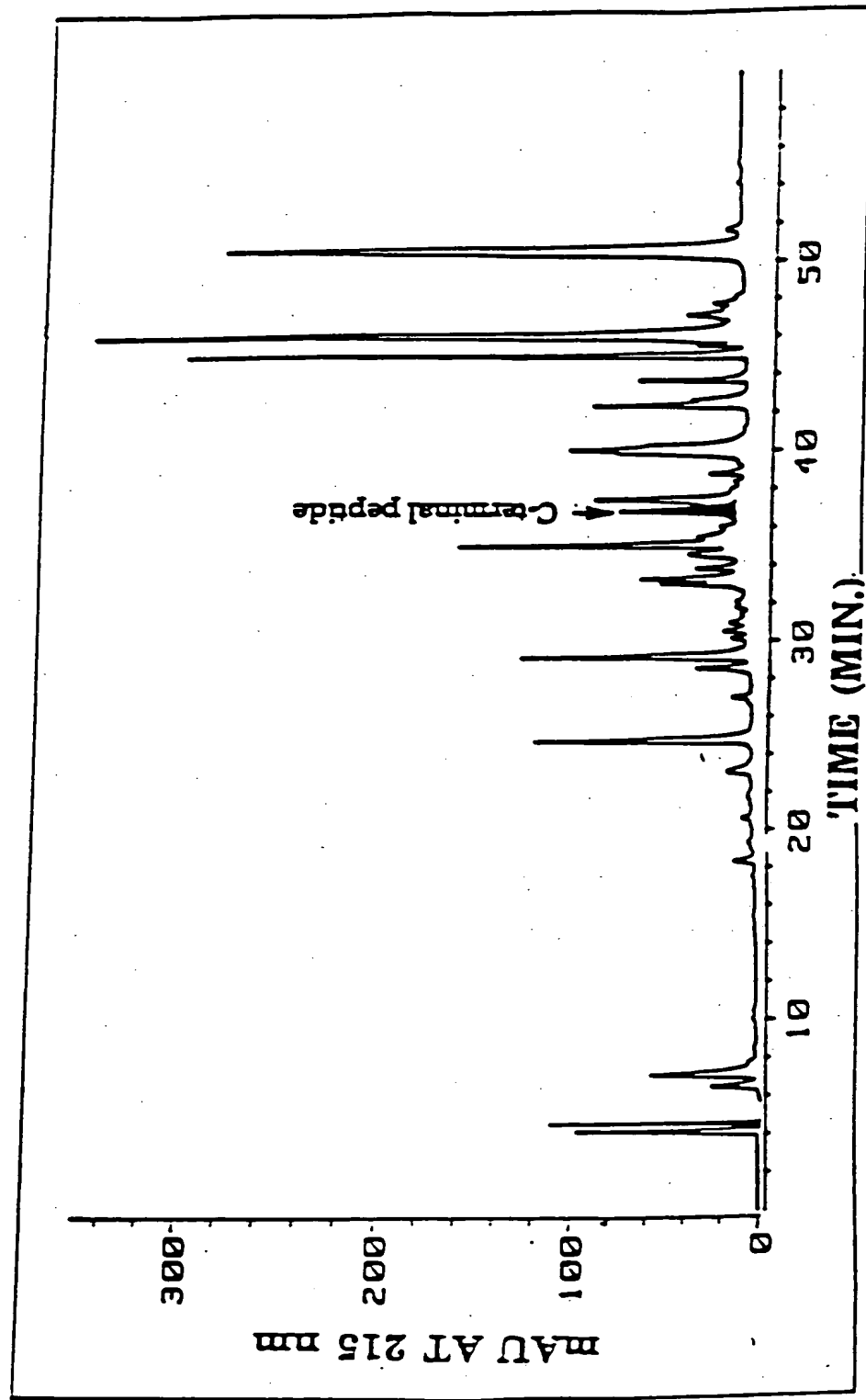


FIG. 16D

EcoRI

ta a t t taa t t c g t a
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
 E F F R I F N R S I D A F K D F V

g a t tagt t t g t a at aag t g
 GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA
 V A S E T S D C V V S S T L S P E

BstEII

t a a cagt c a a t t a c t . a
 AAAGACTCCCGTGTTTCGGTTACCAACCGTTTCATGCTGCCGCCGGTTGCT
 K D S R V S V T K P F M L P P V A

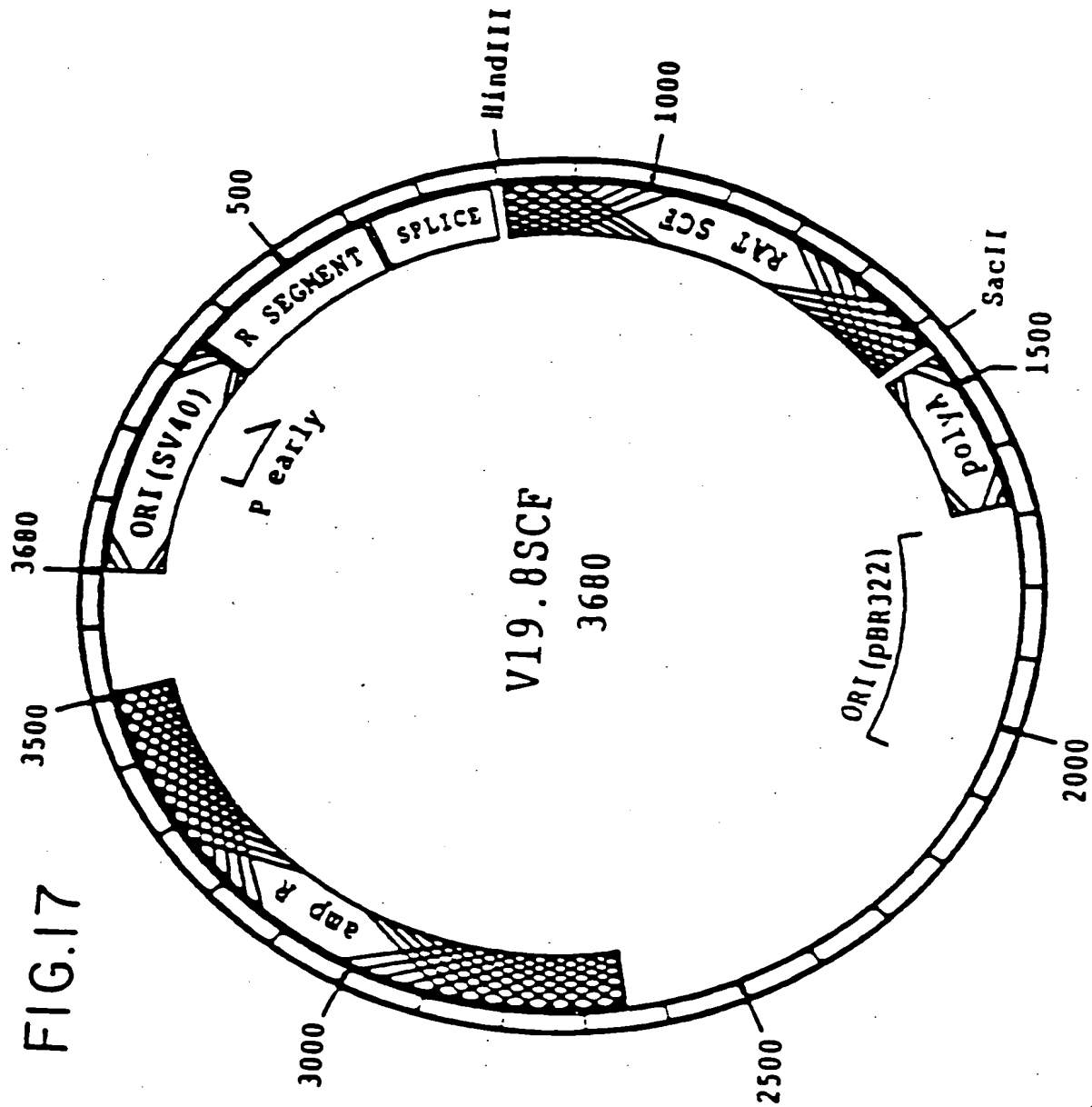
cag tag t ag agtag agt tagt g a t
 GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACCTCCAAATACATCTAC
 A S S L R N D S S S S N S K Y I Y

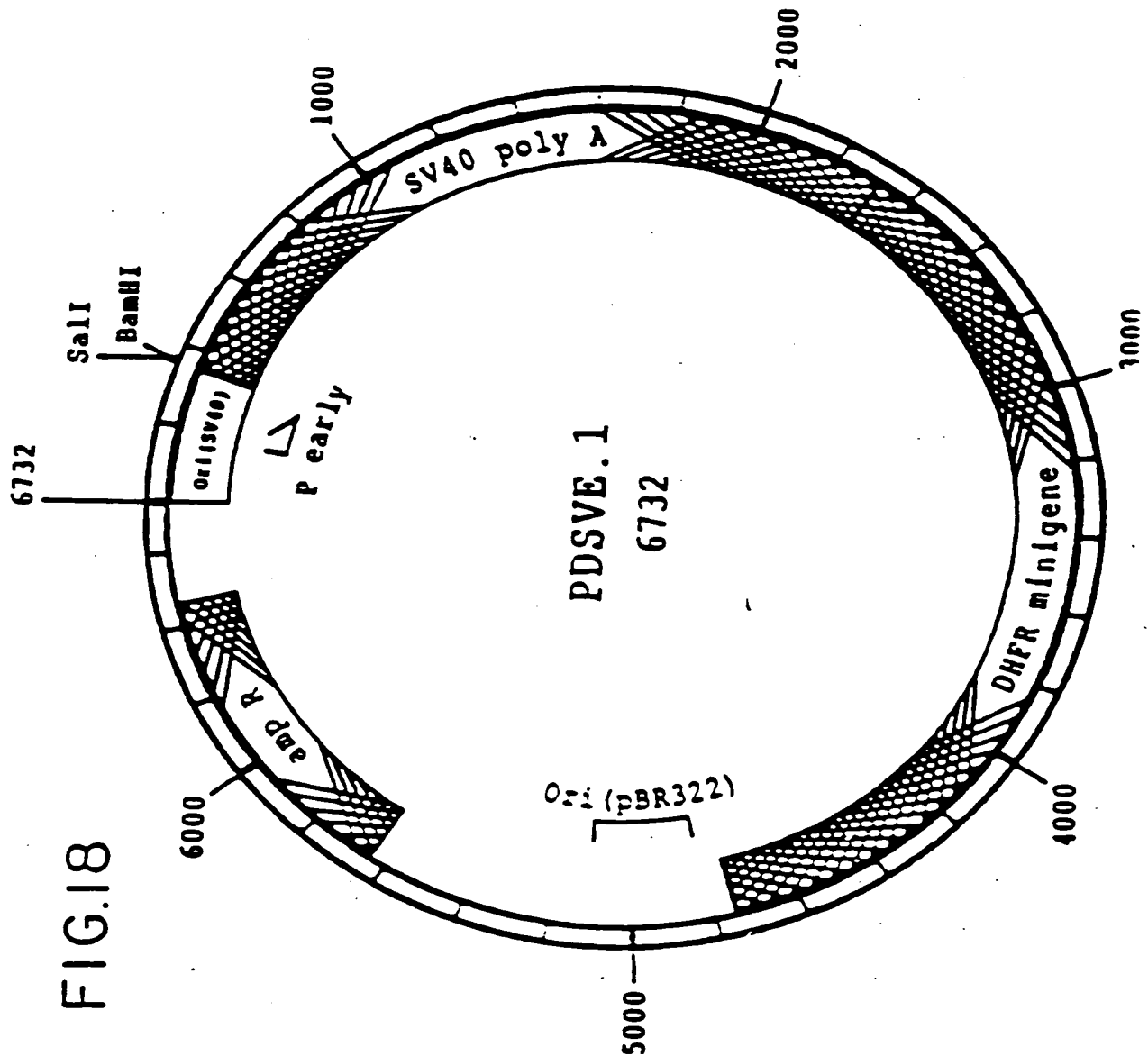
BamHI

t
CTGATCTAATAGGATCC
 L I . .

FIG. 16E

BstEII
GGTTACCAAACCGTTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC BamHI
V T K P F M L P P V A A . .





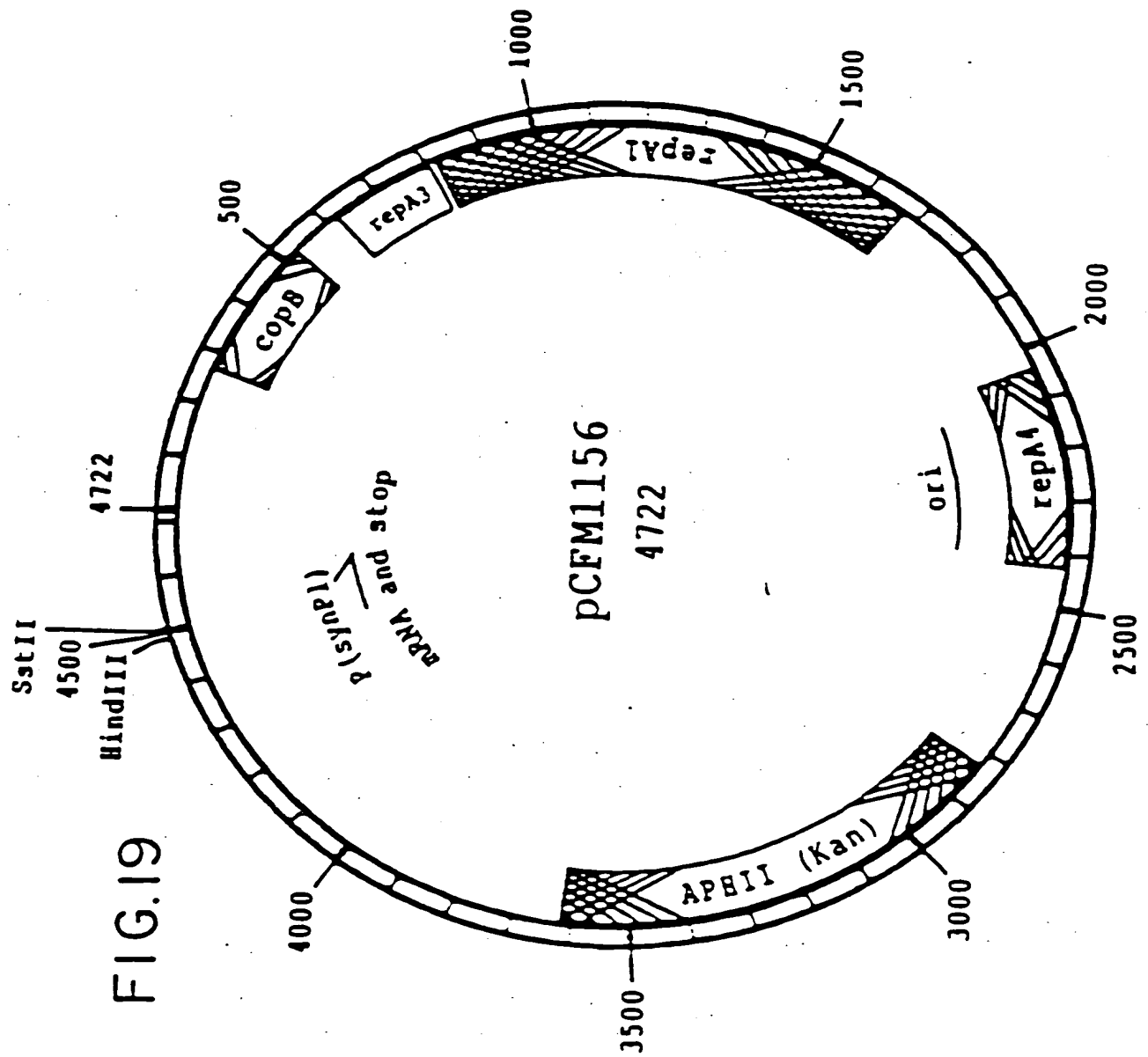


FIG.20A

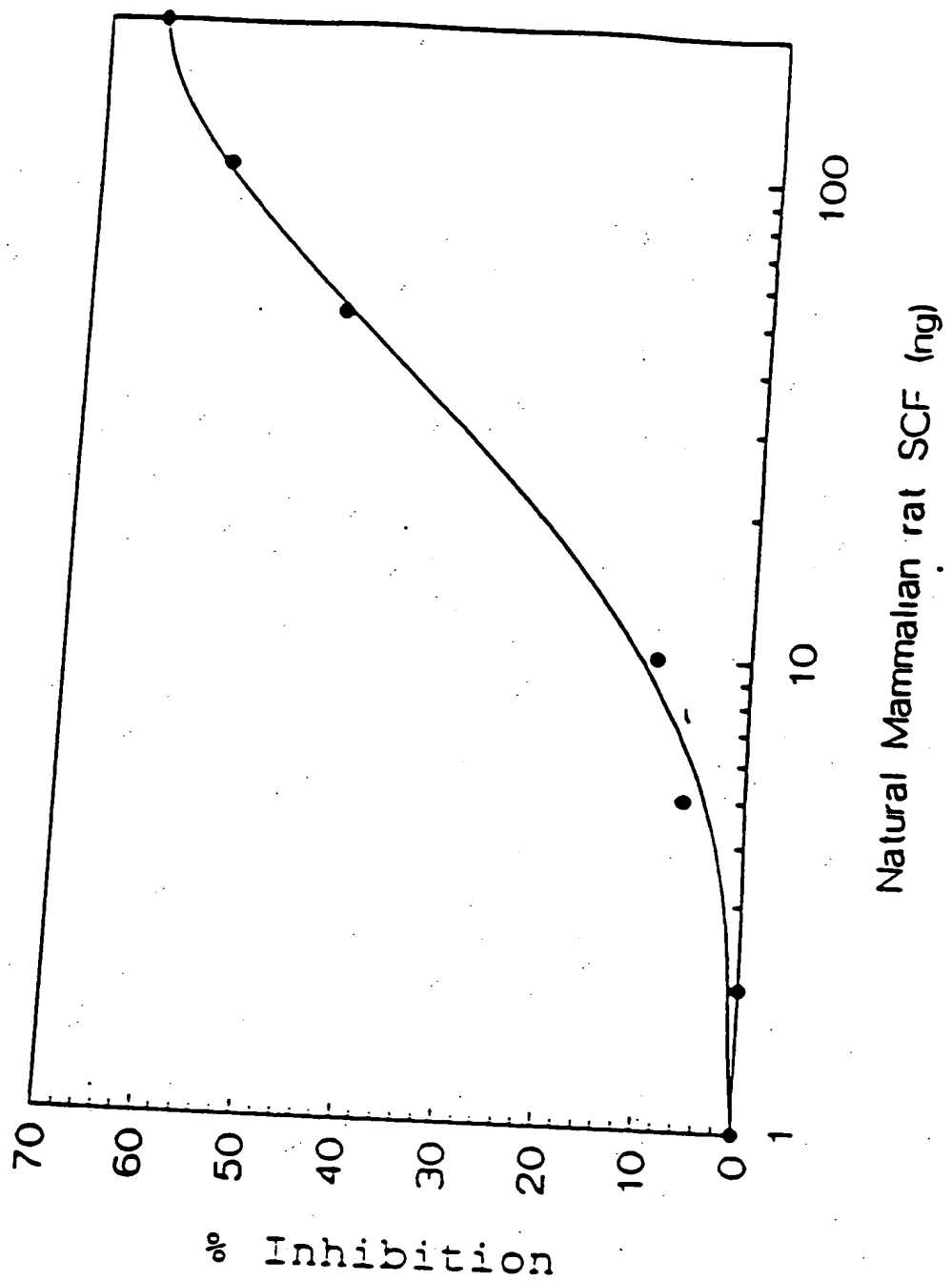


FIG. 20B

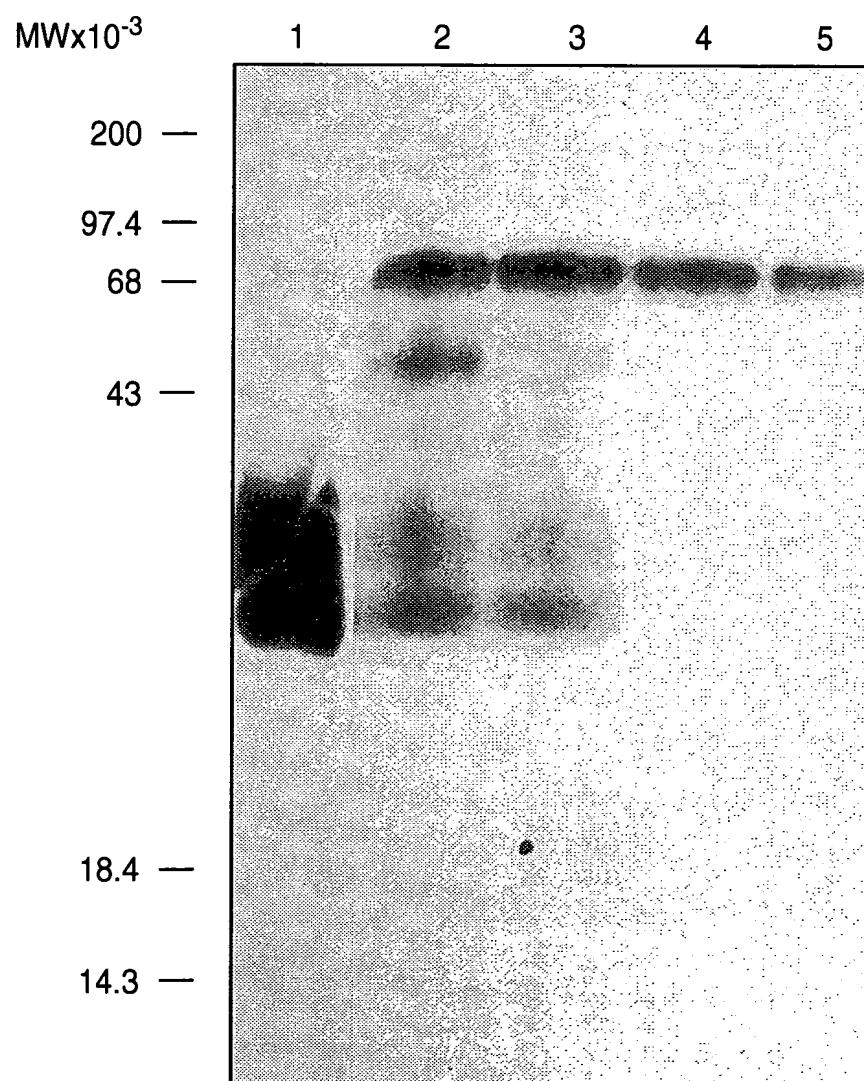


FIG. 21

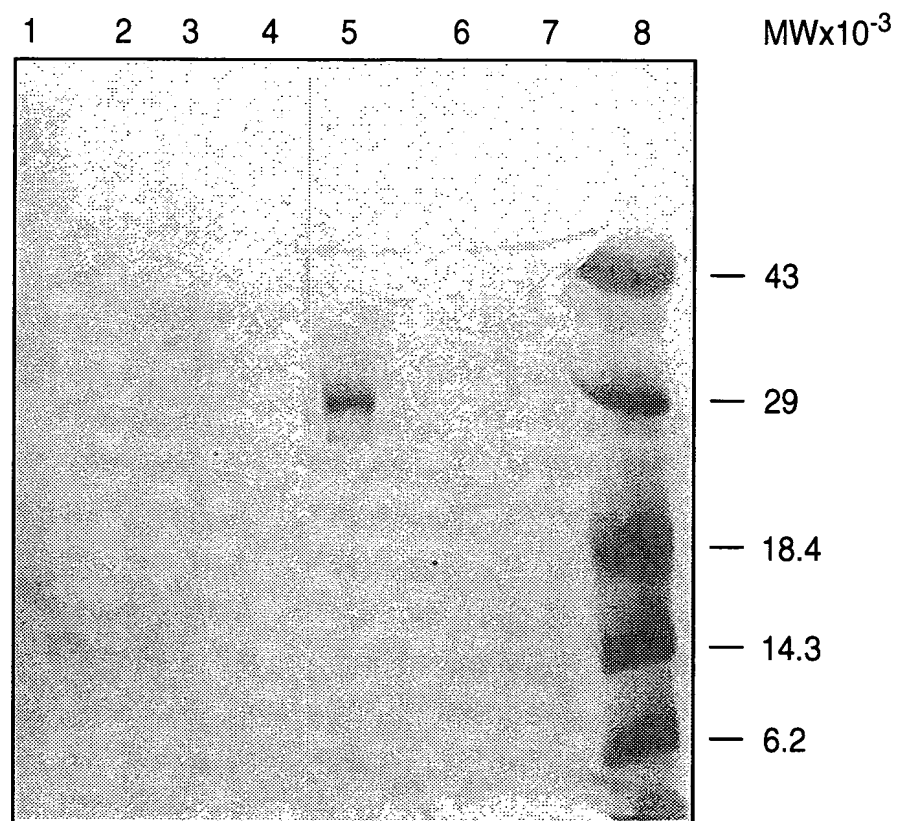


FIG. 22

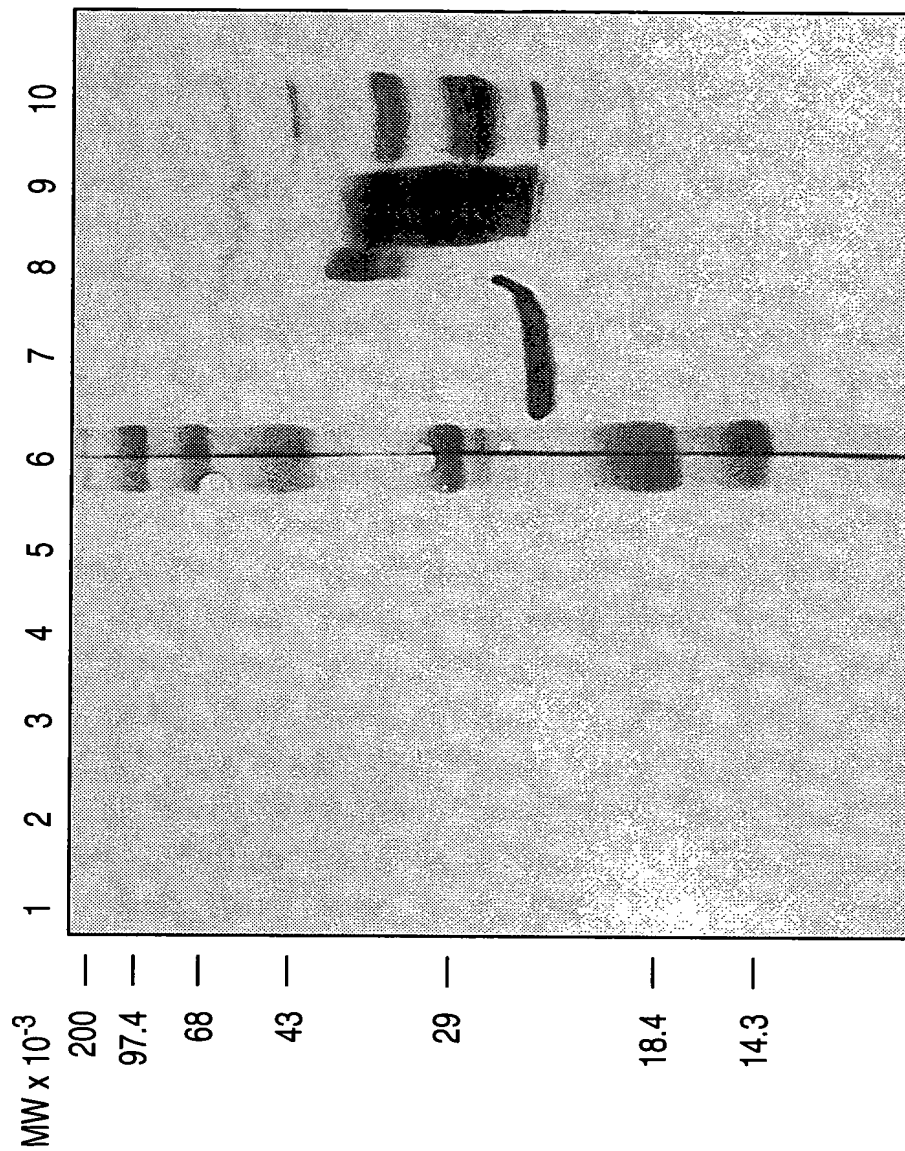


FIG. 22A

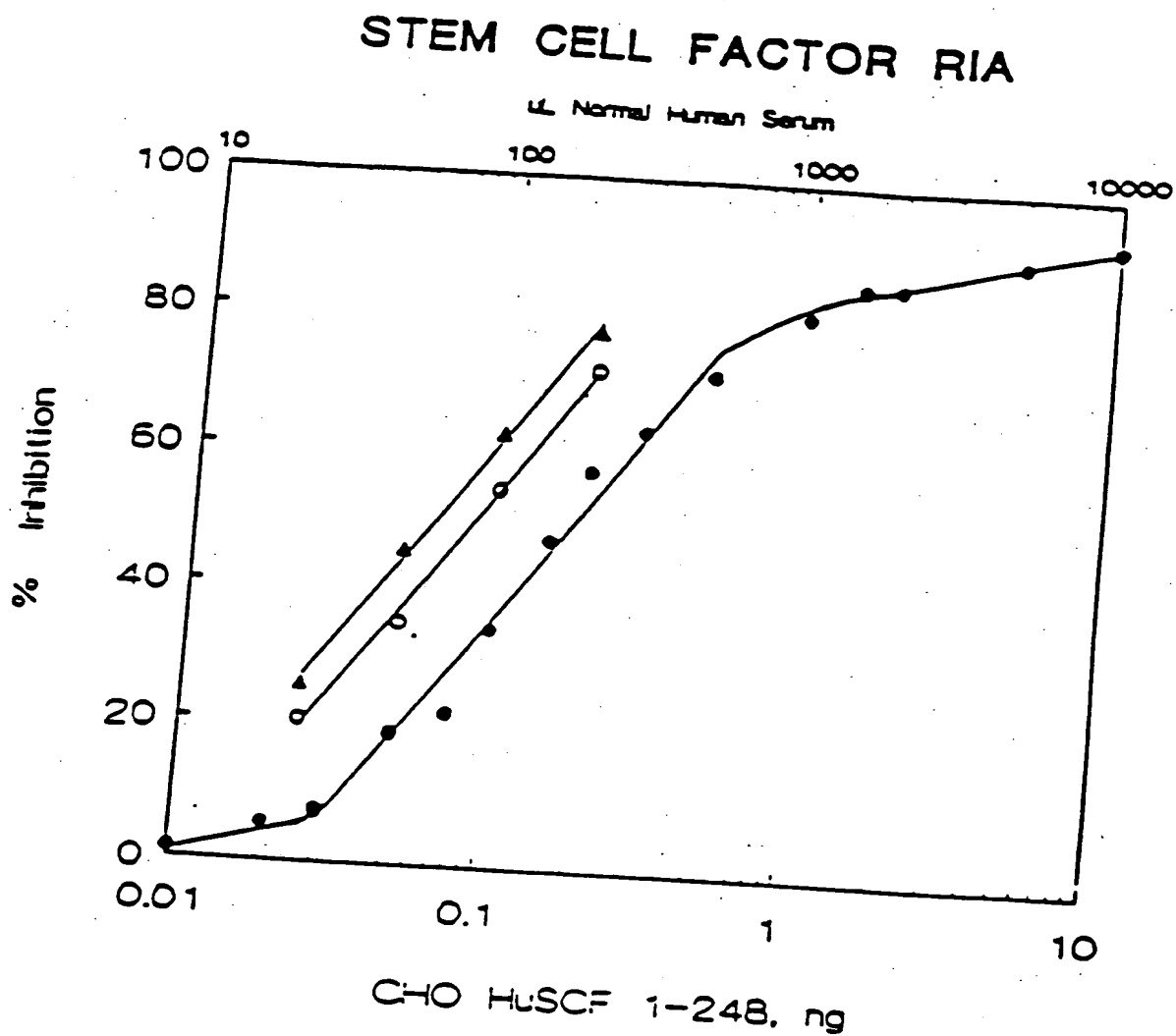
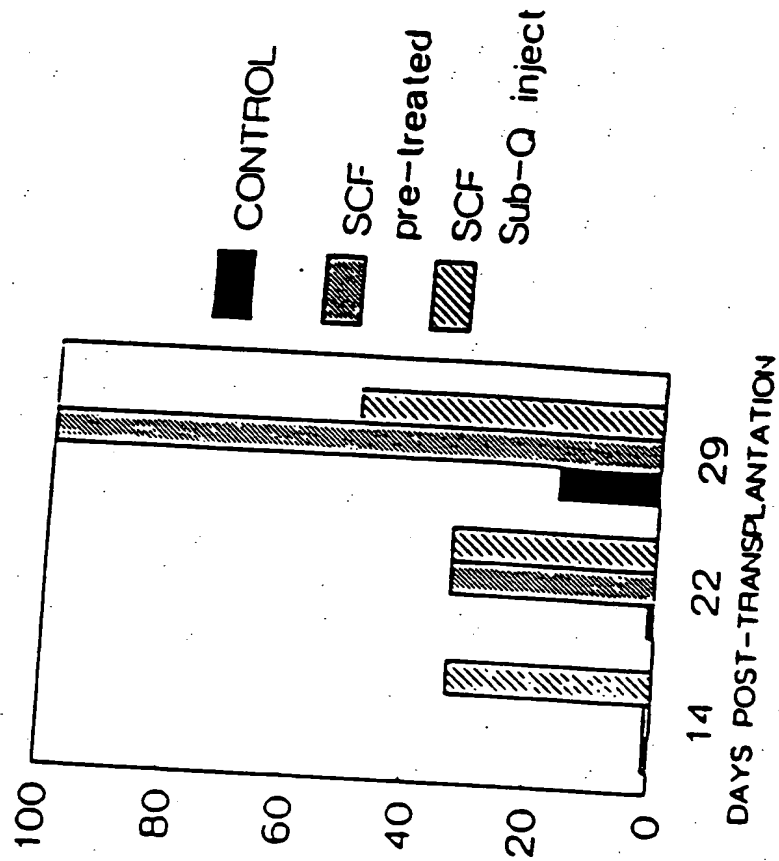


FIG. 23



% MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A

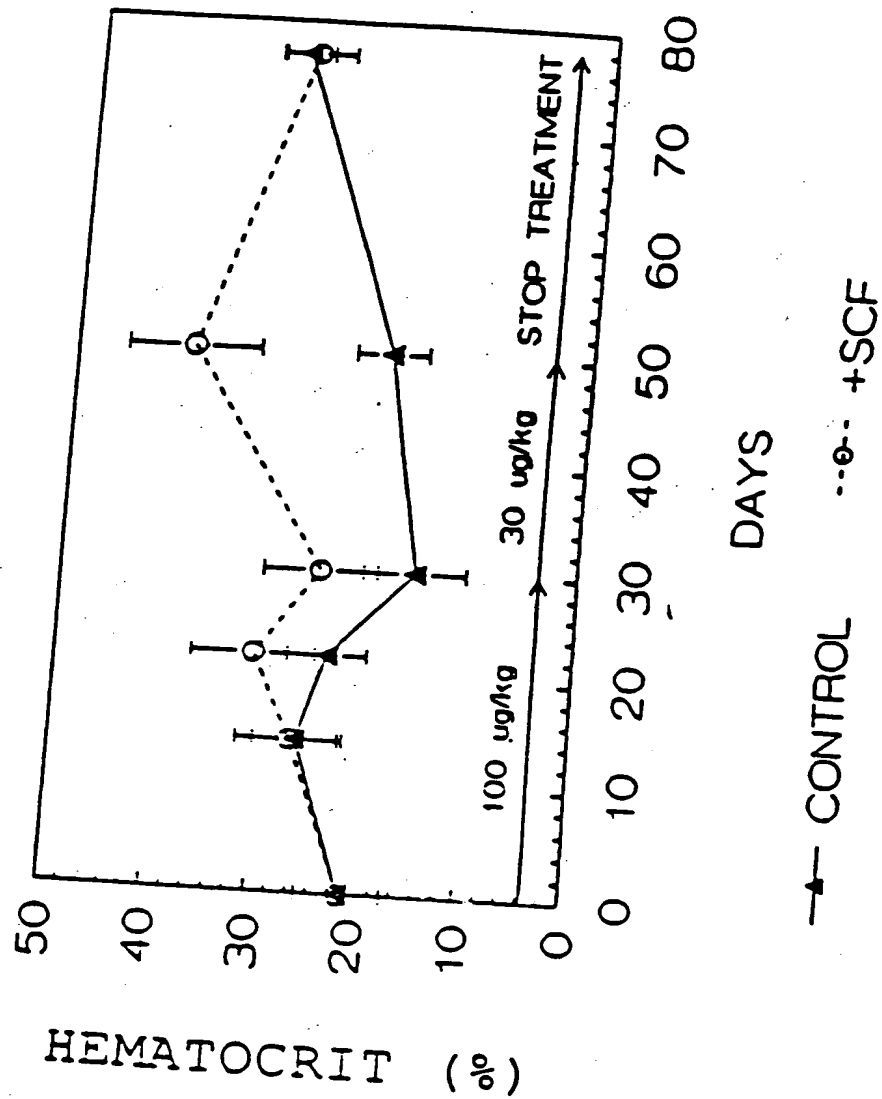


FIG. 24B

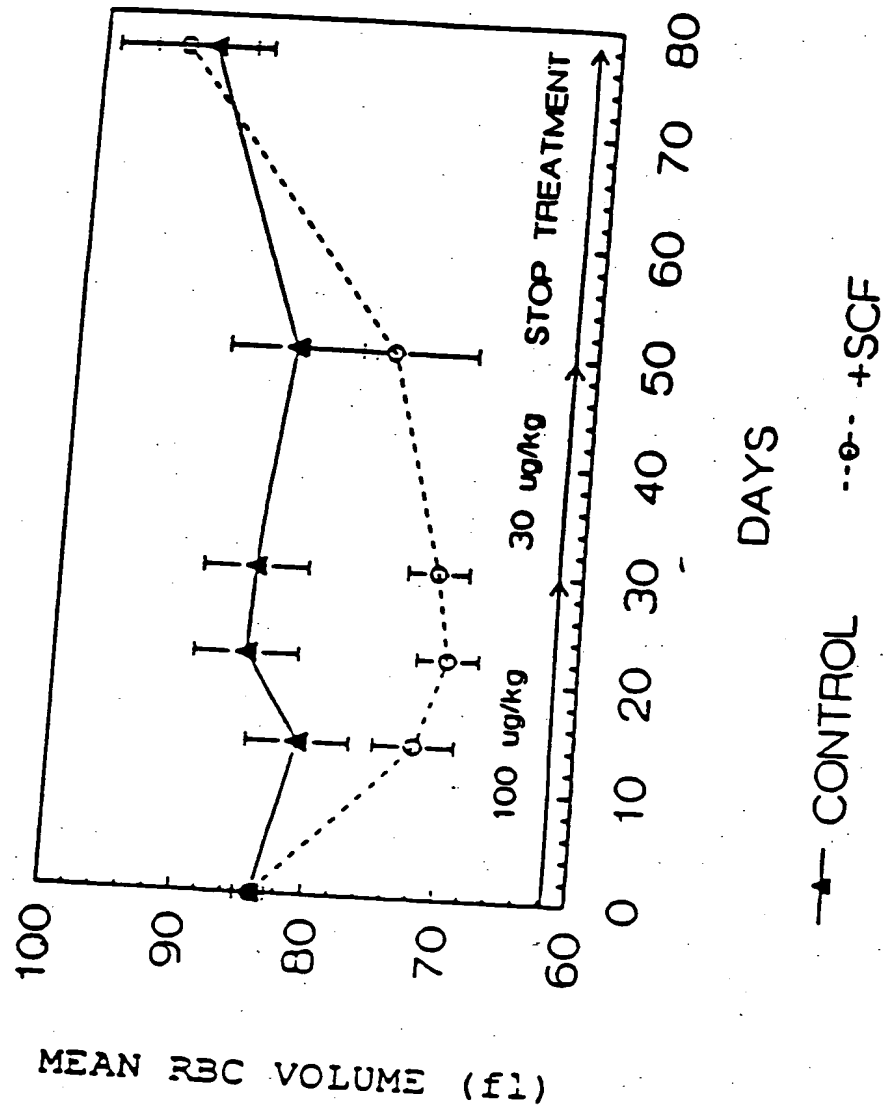


FIG. 25

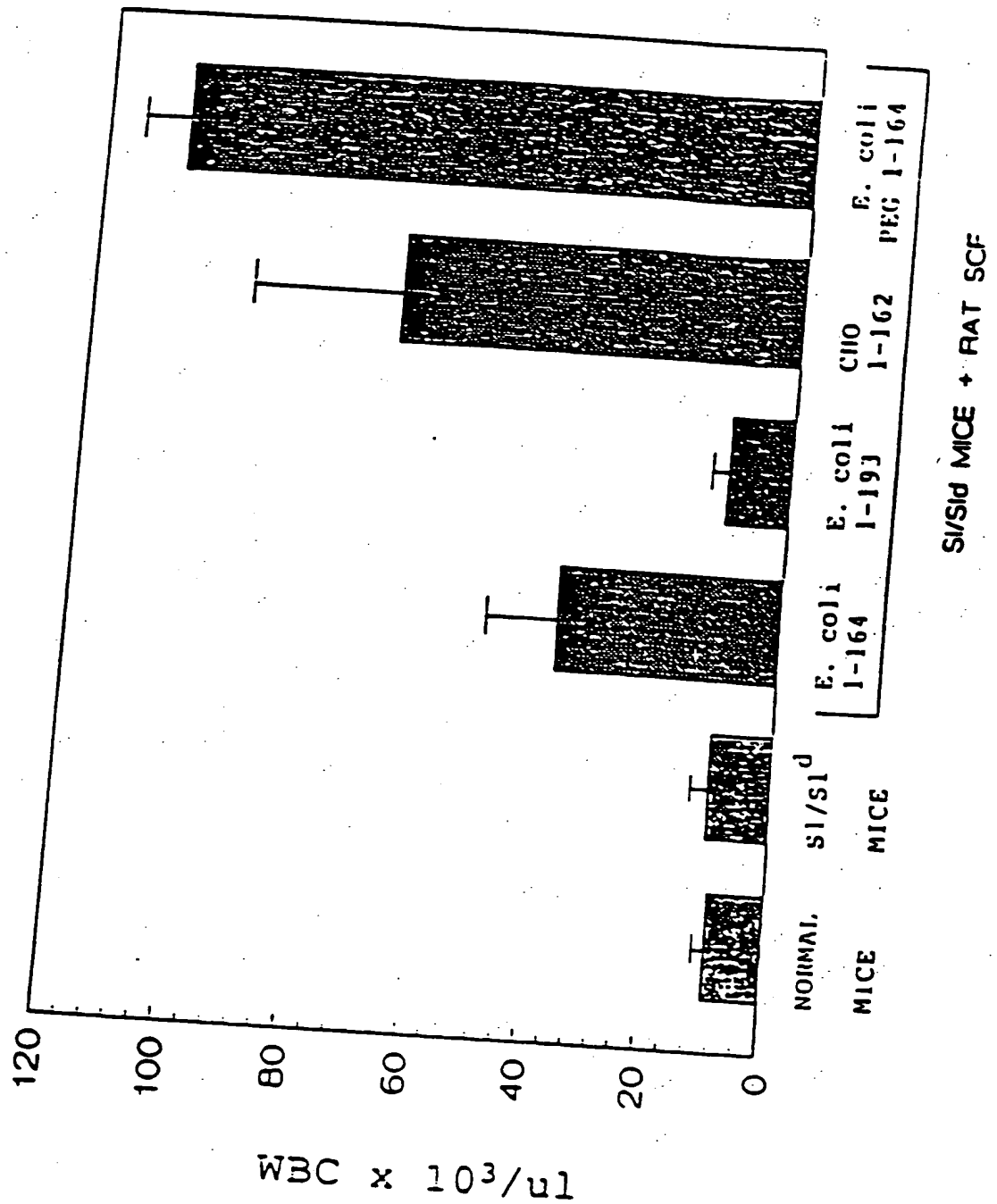


FIG. 26

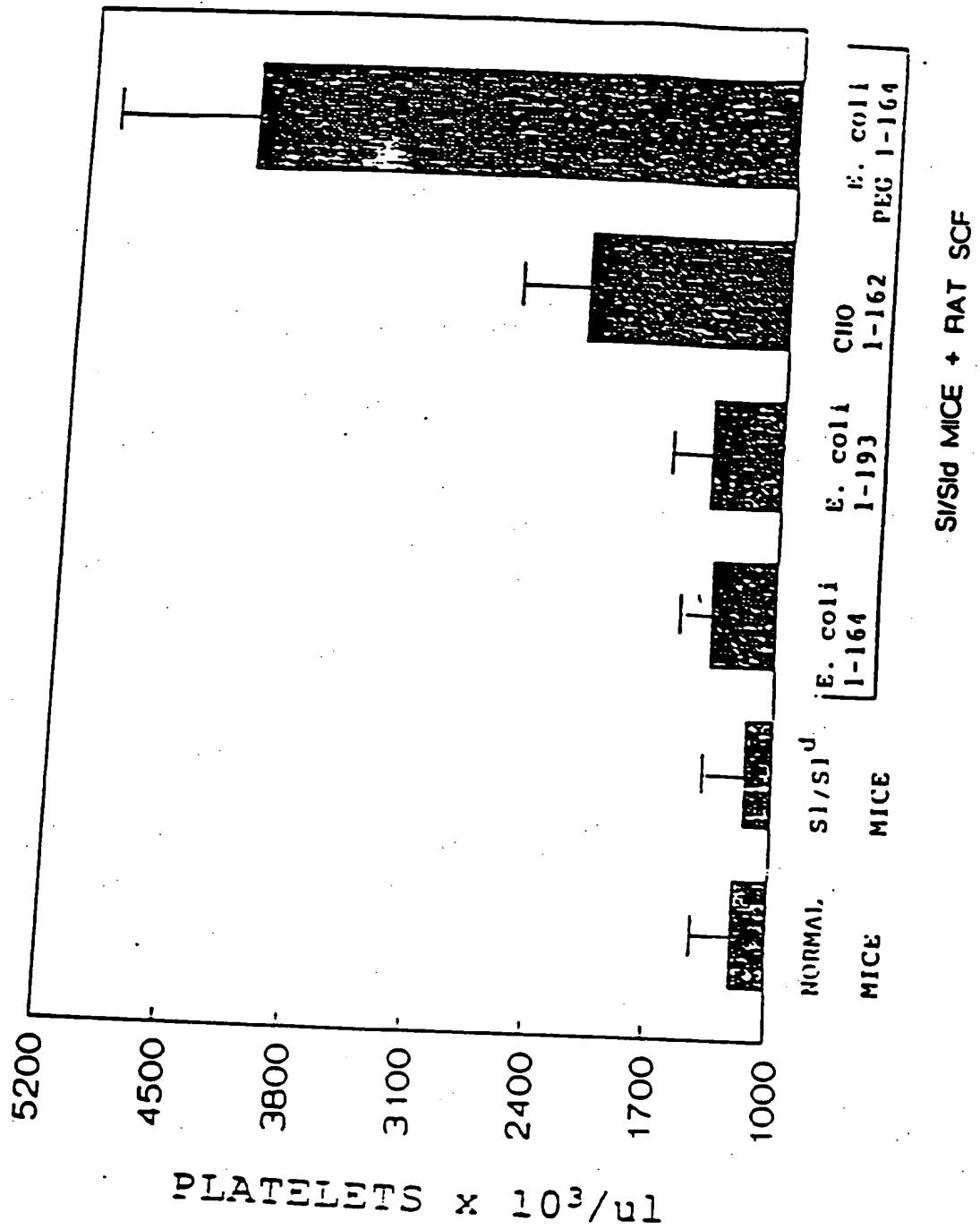


FIG. 27

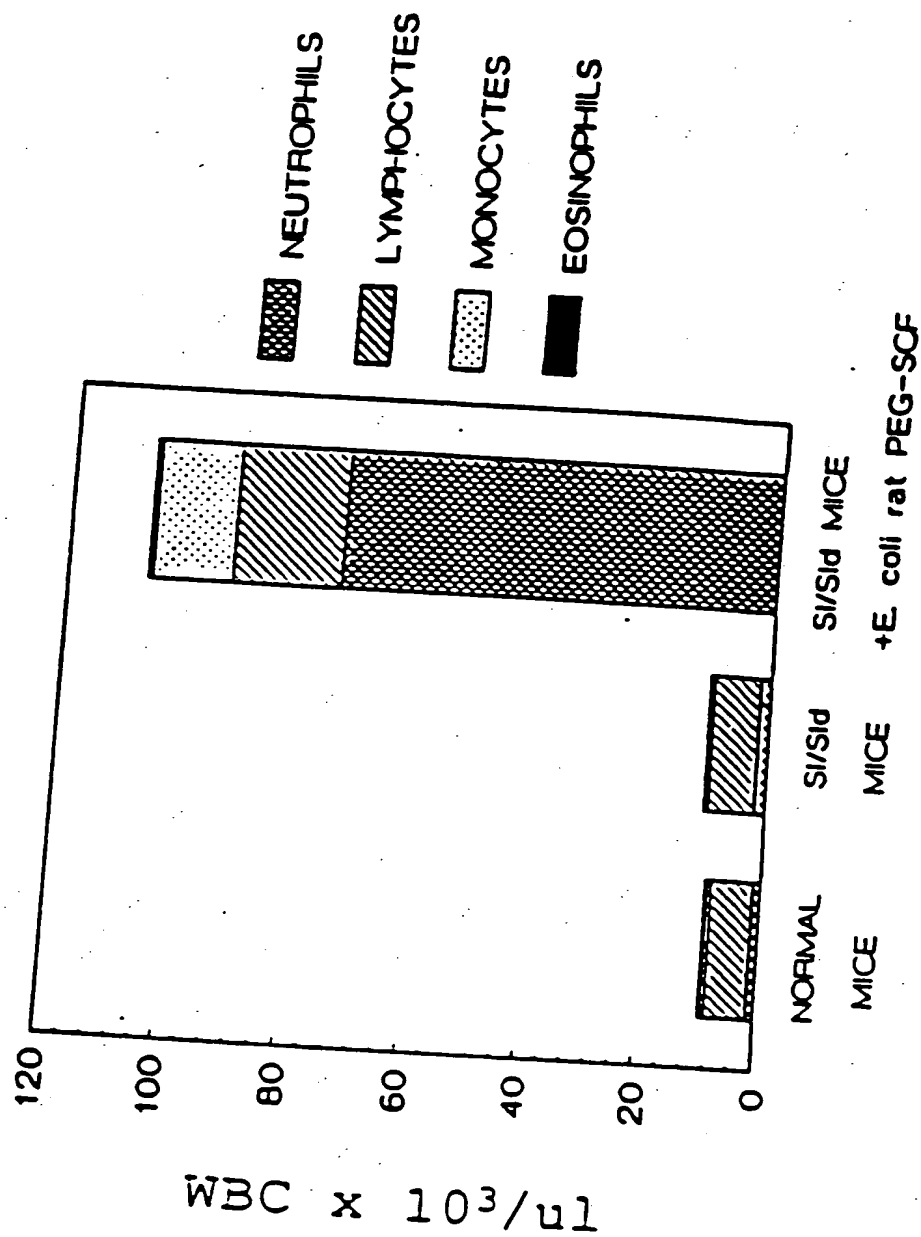


FIG. 28

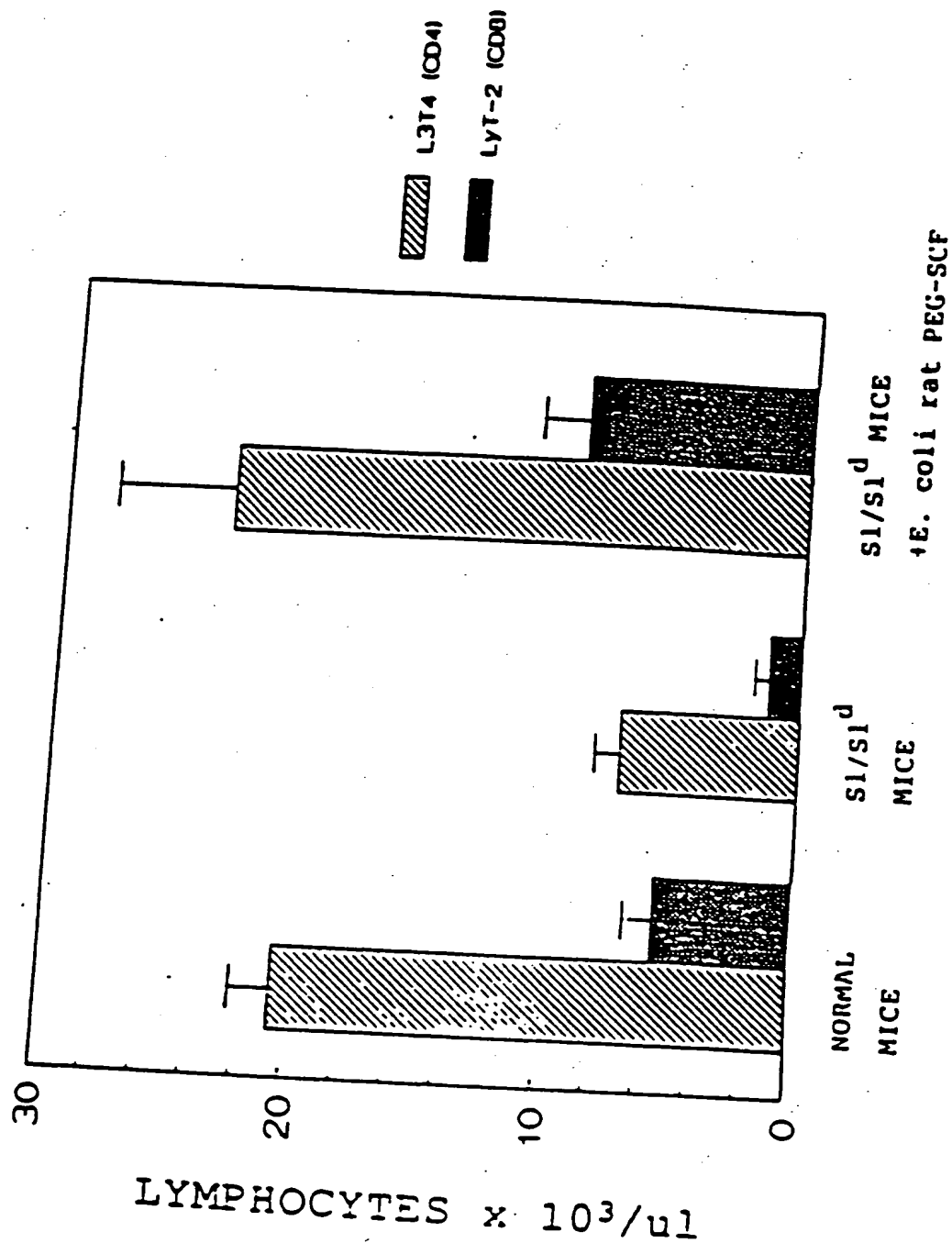
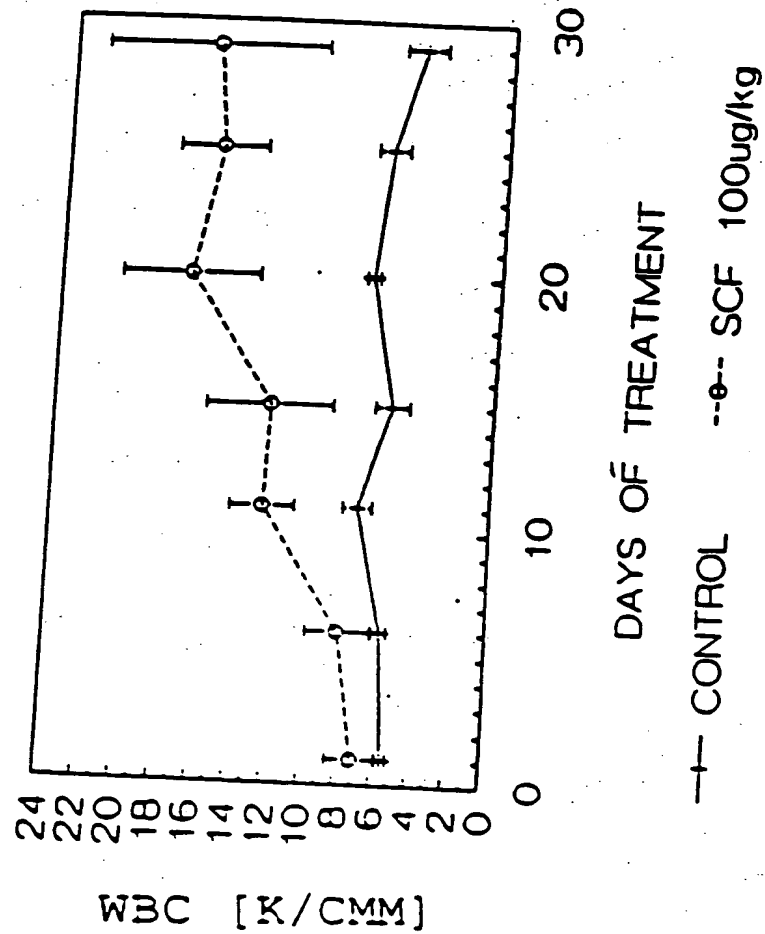
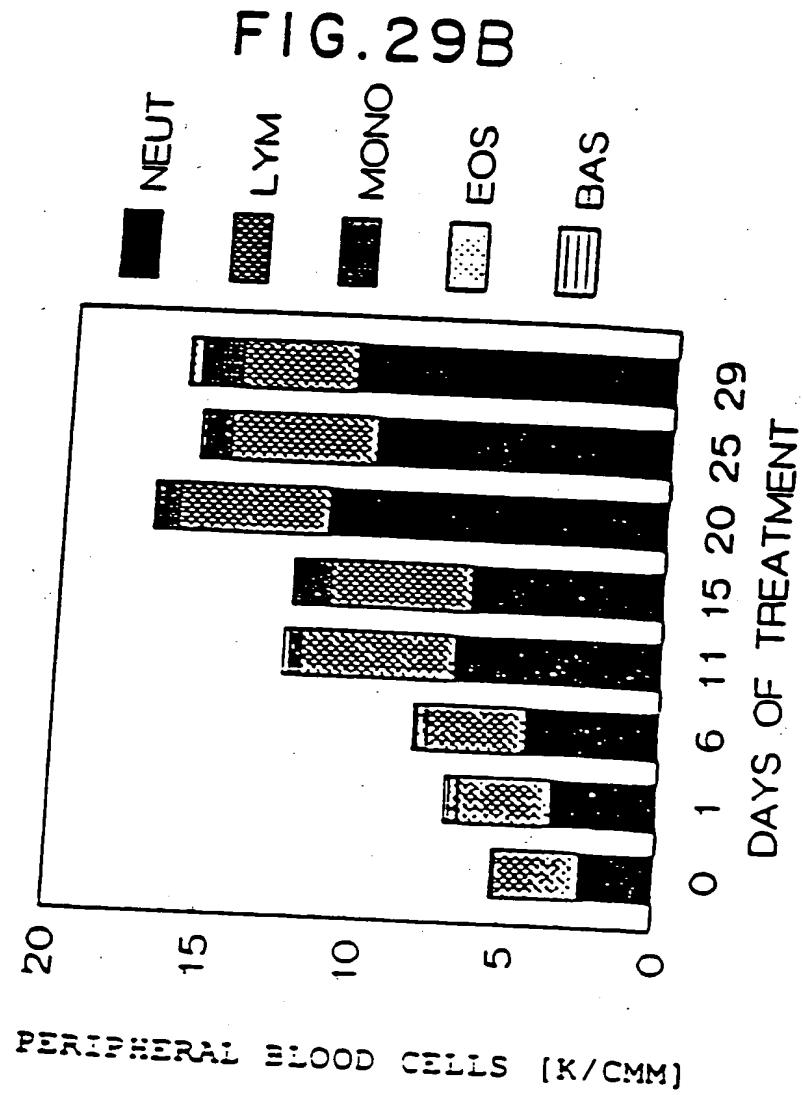
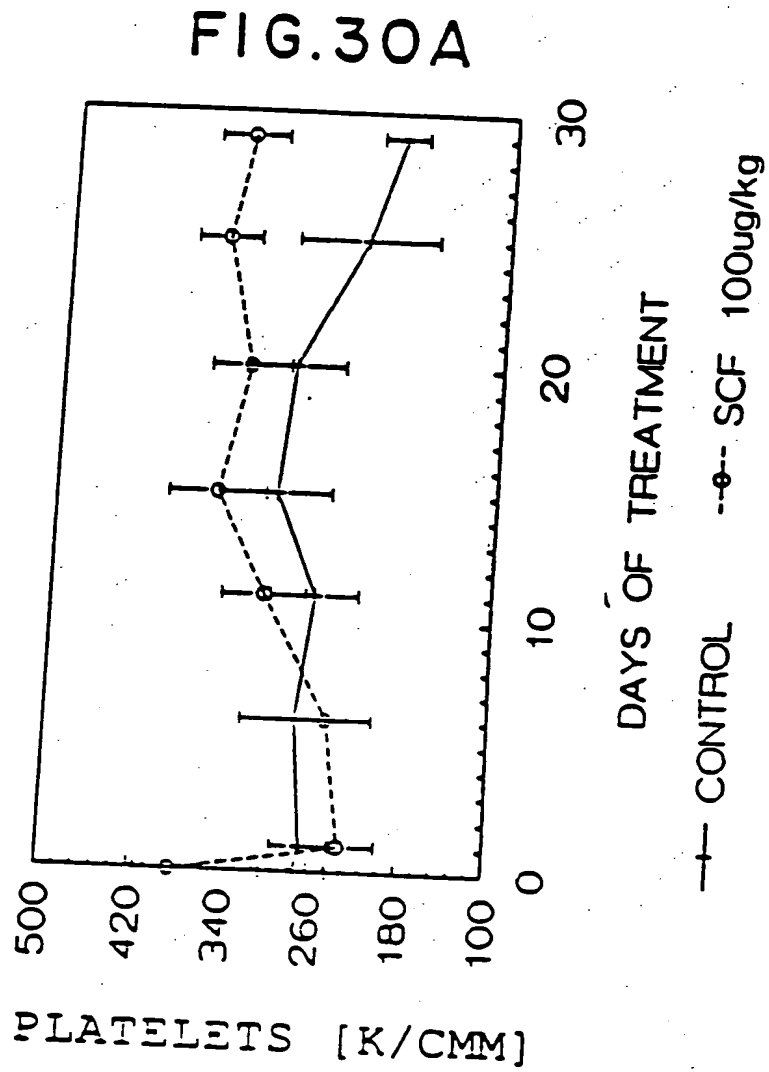


FIG. 29A







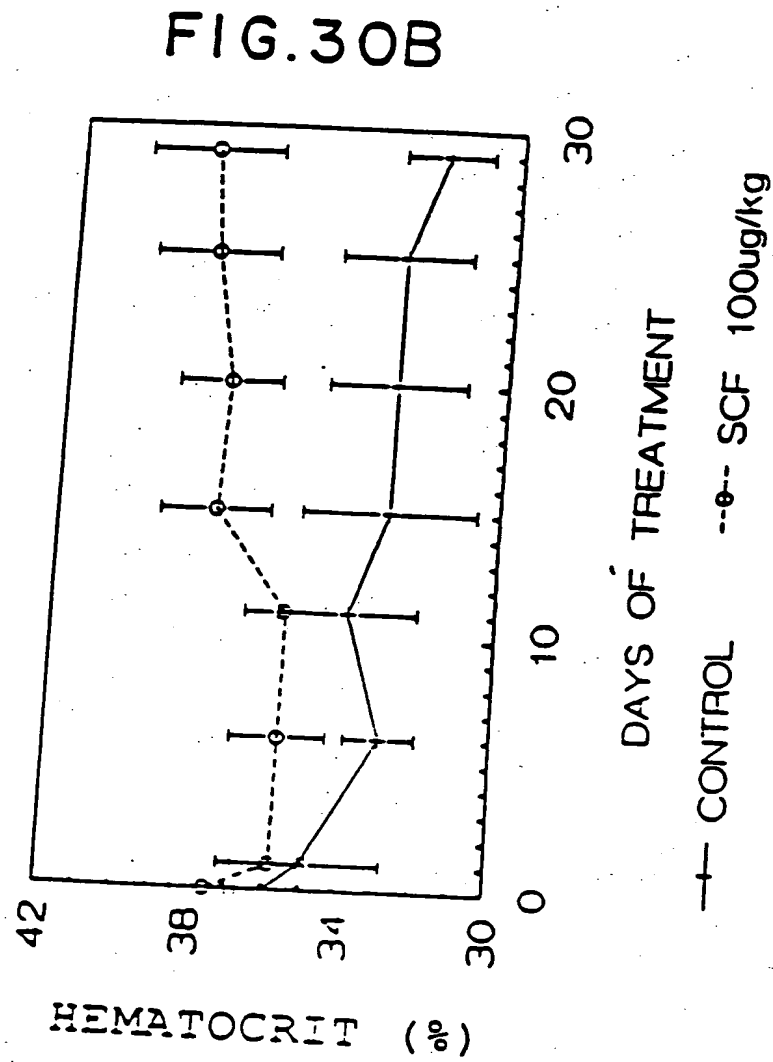


FIG. 31B

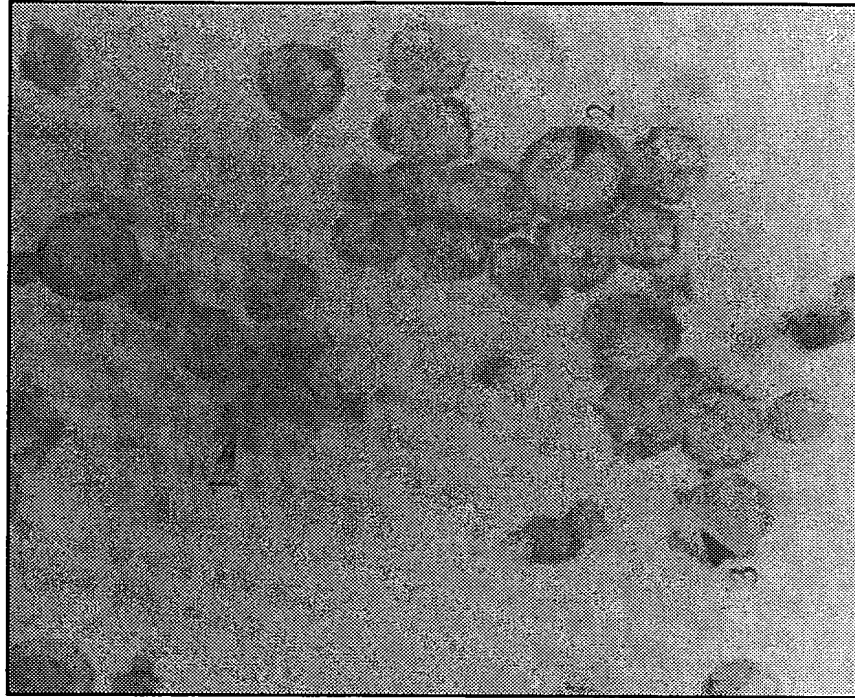


FIG. 31A

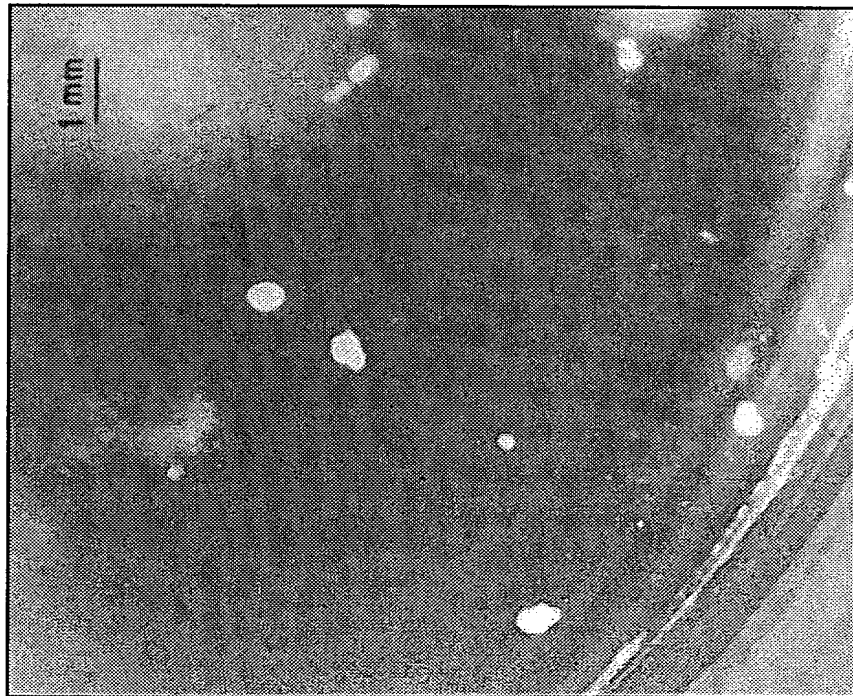


FIG. 31C

SCF4 SMP4

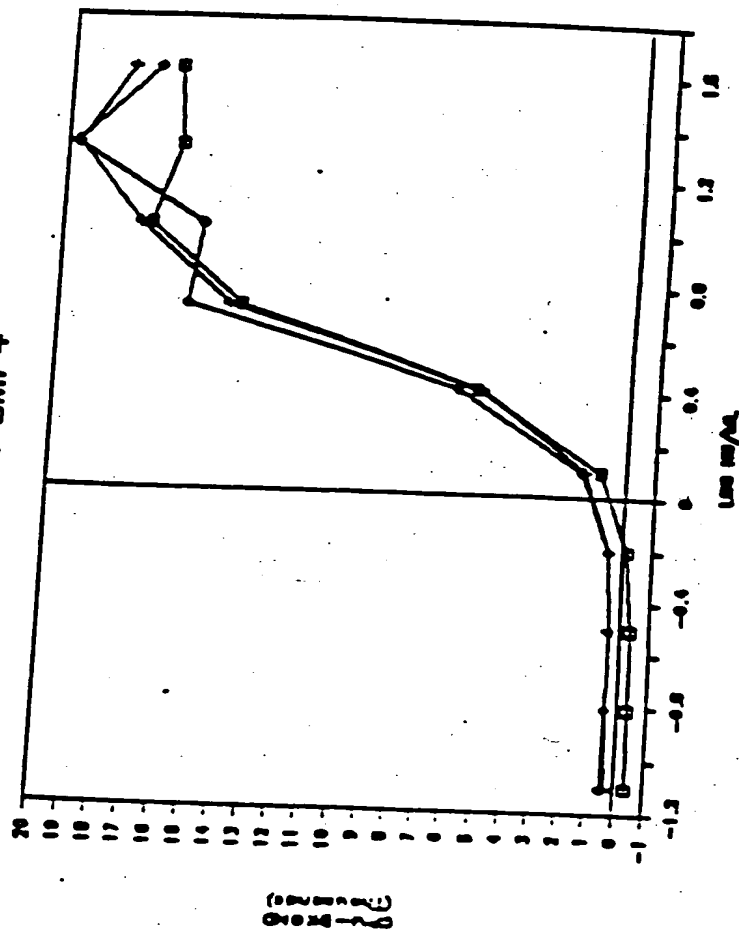


FIG. 32A

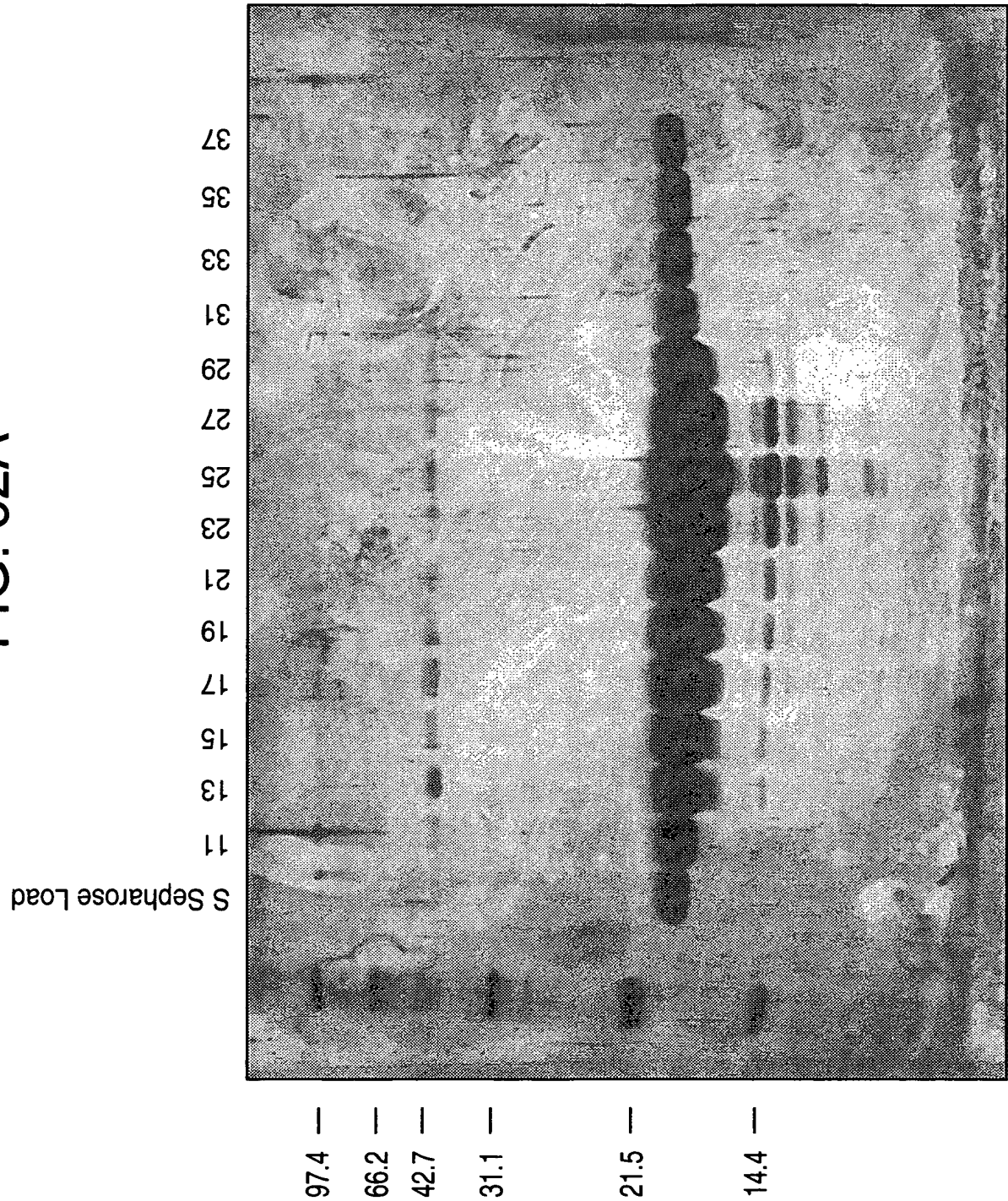


FIG. 32B

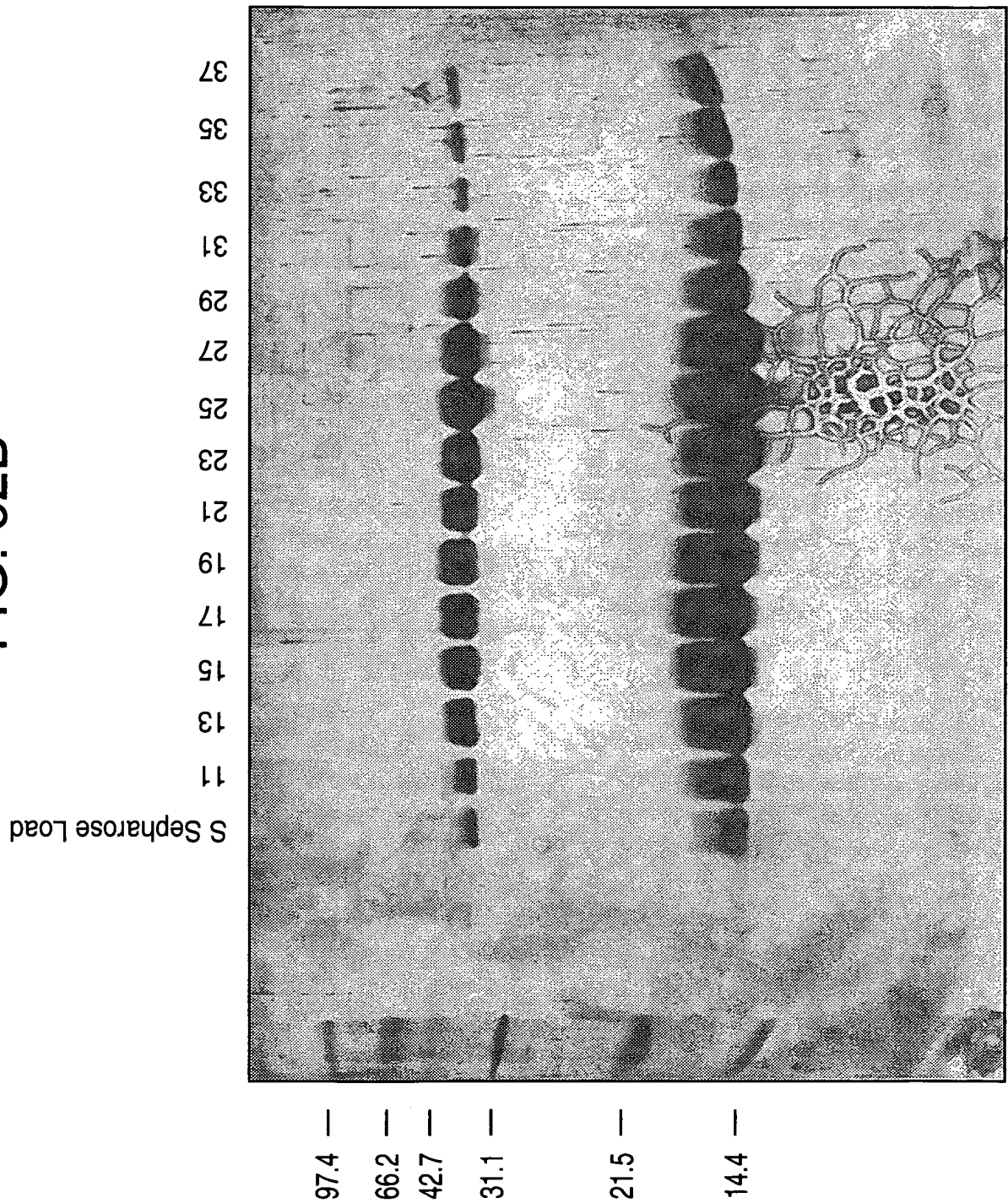


FIG. 33

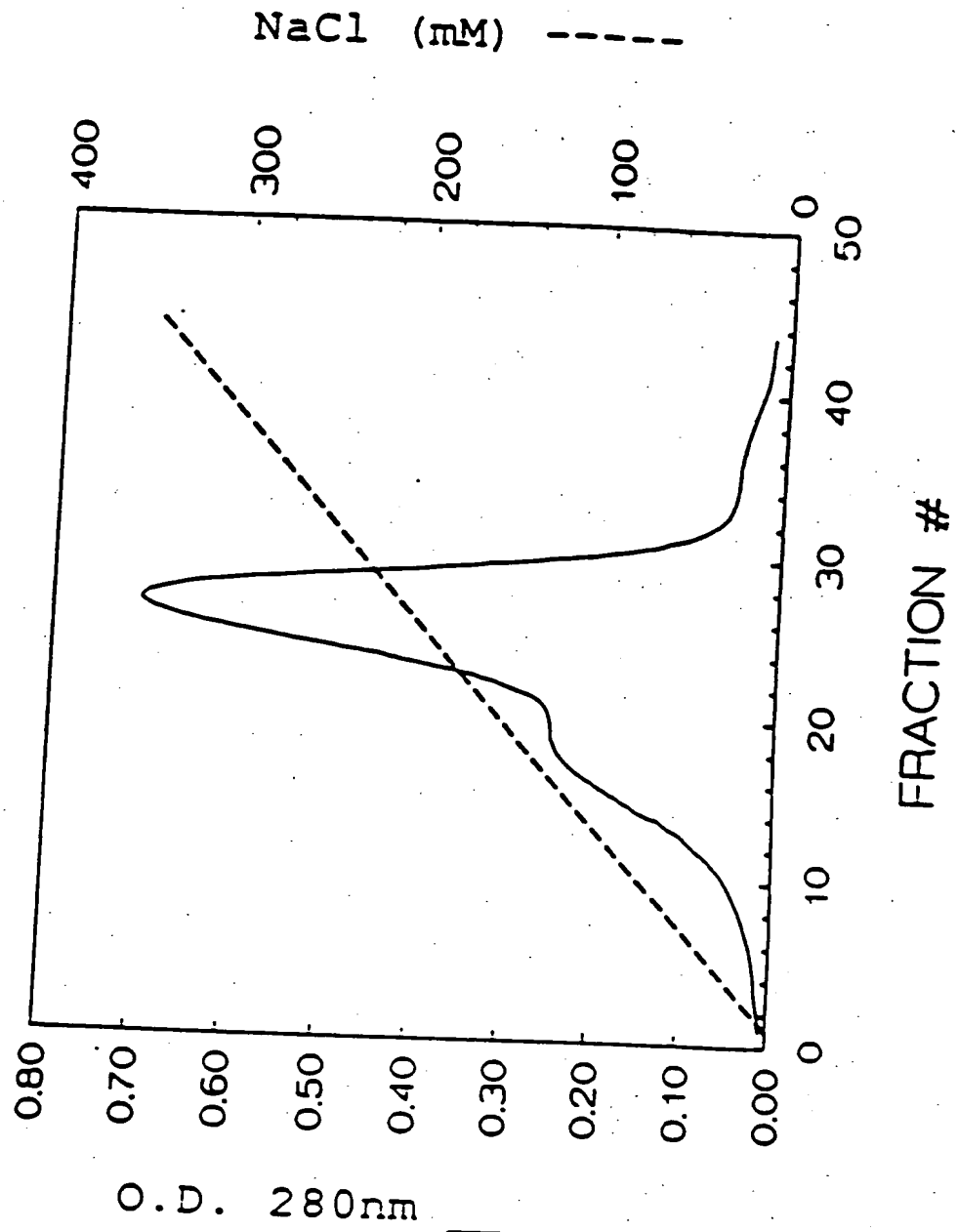


FIG. 34A

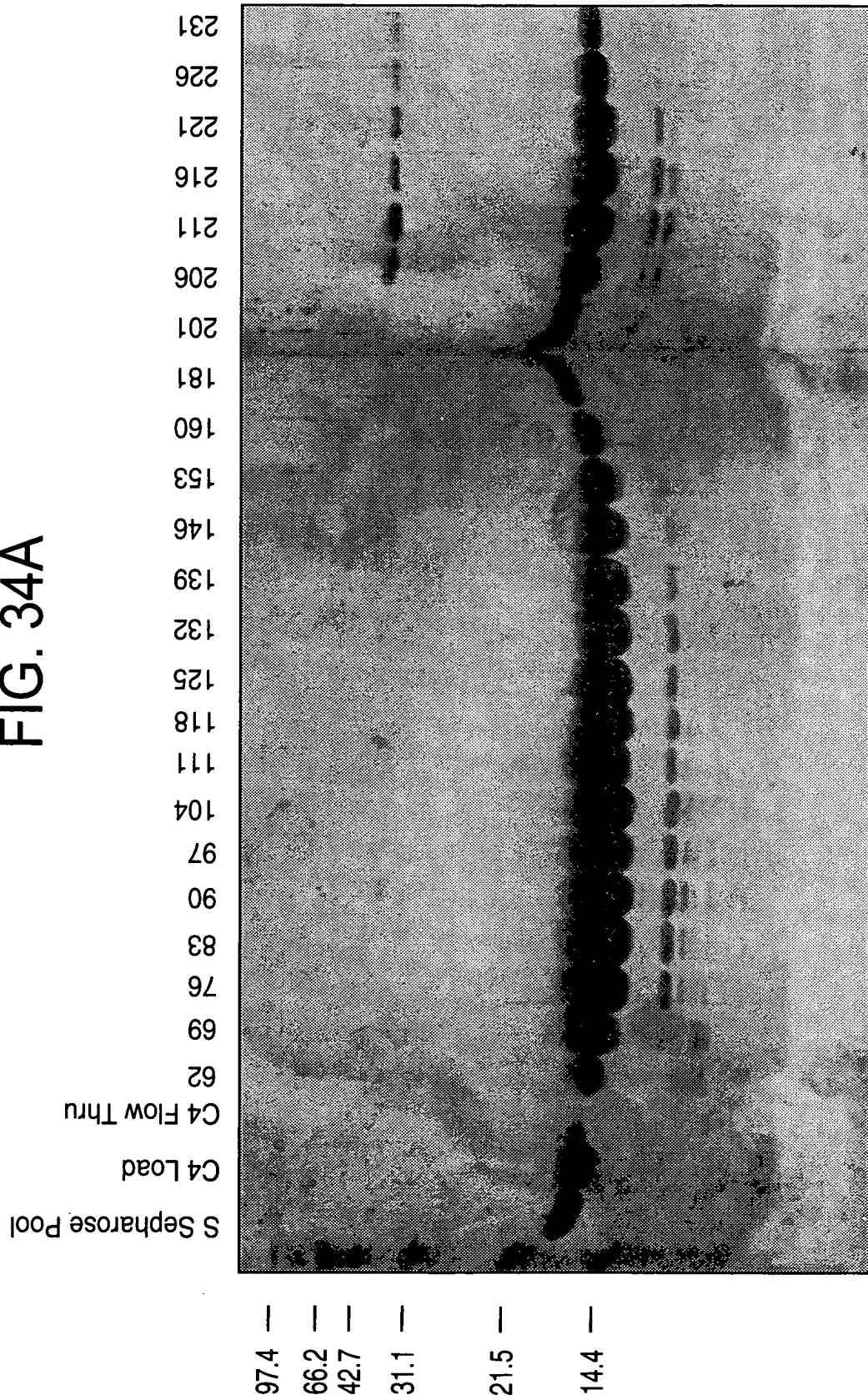
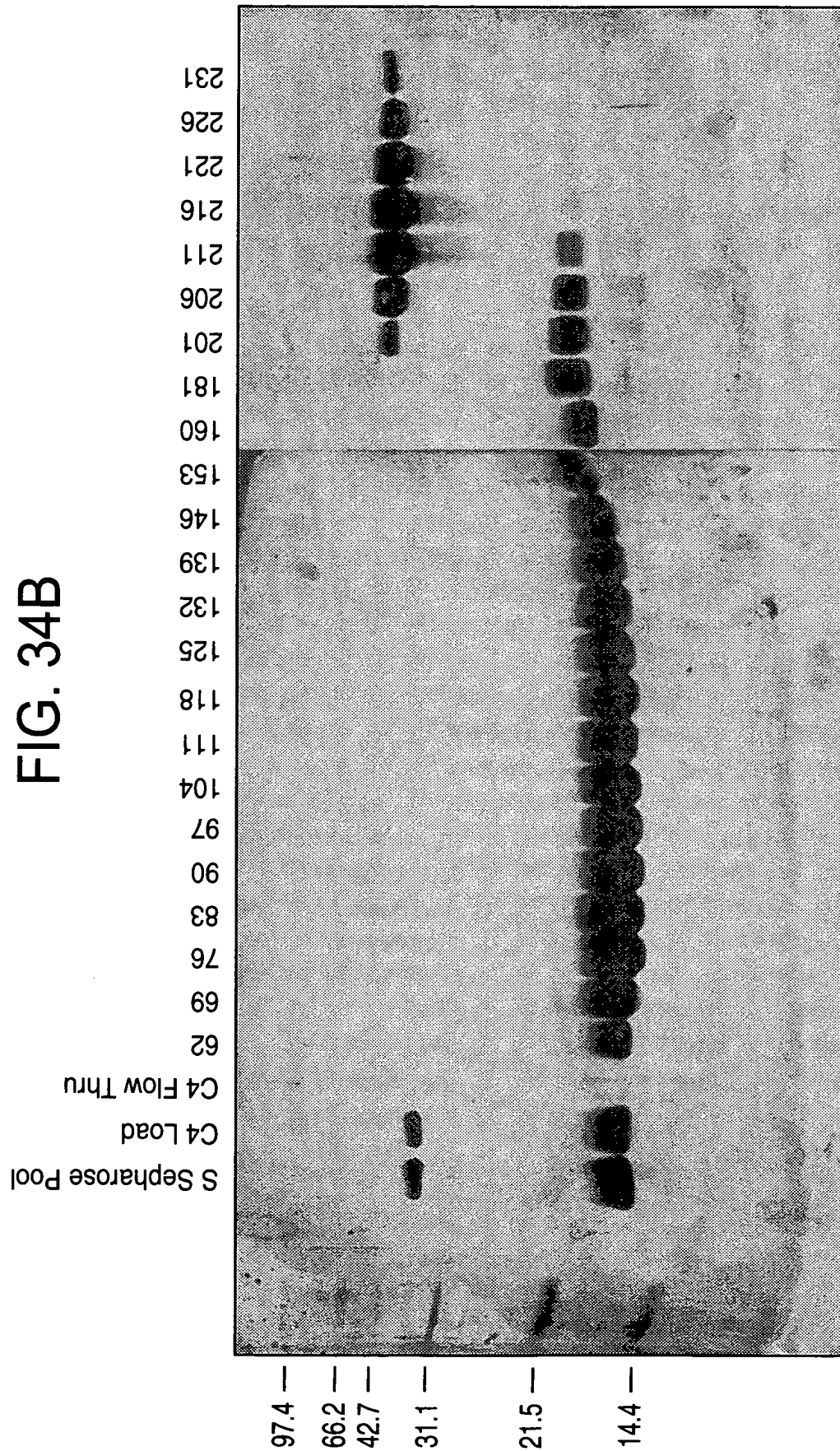
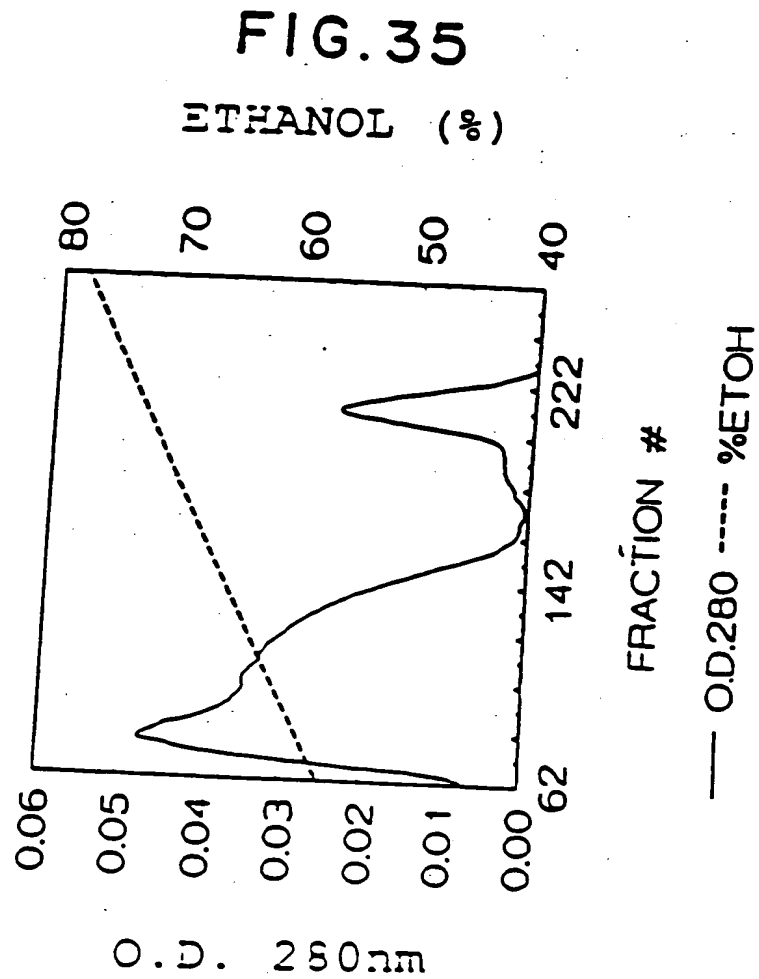
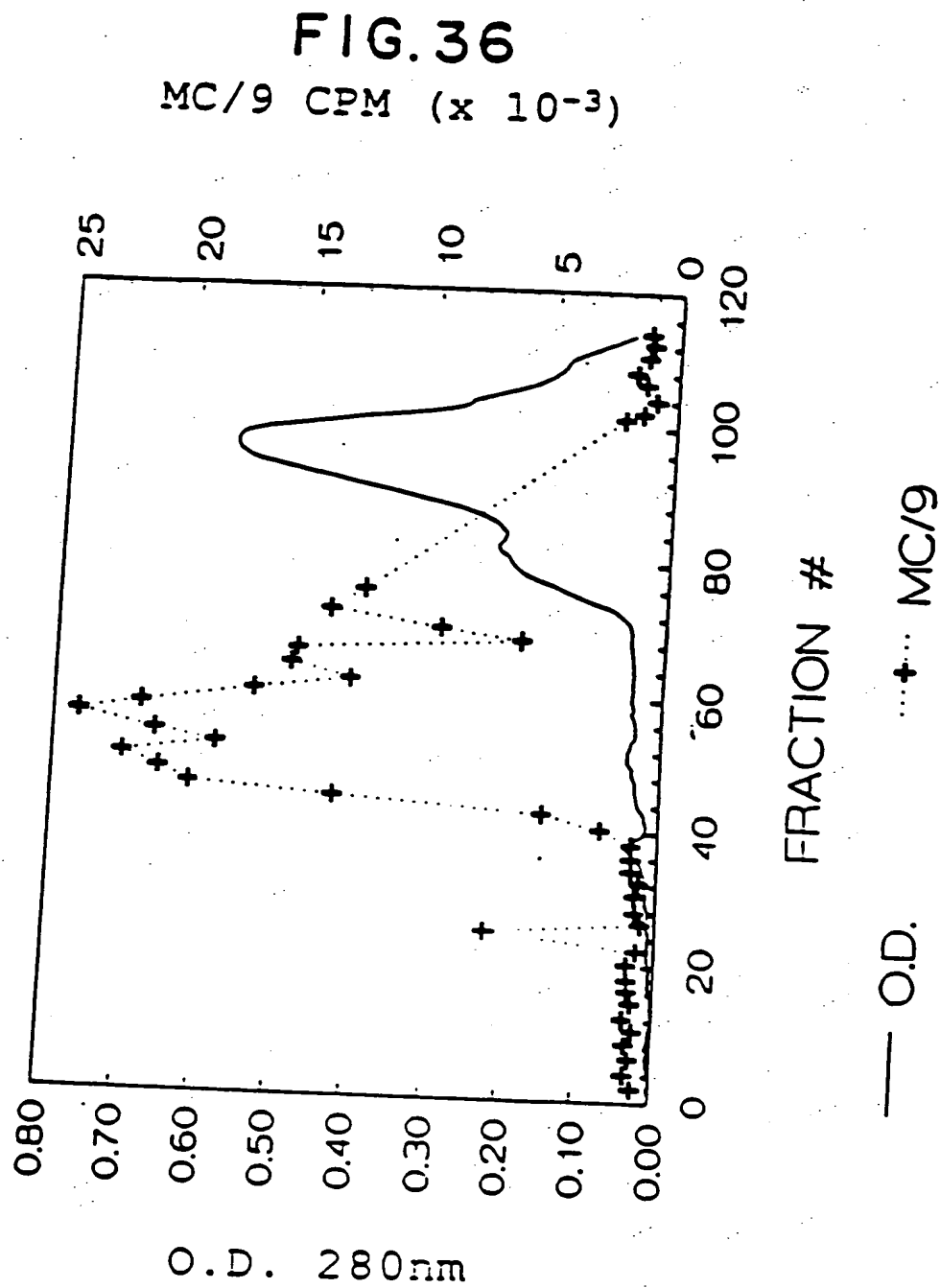


FIG. 34B







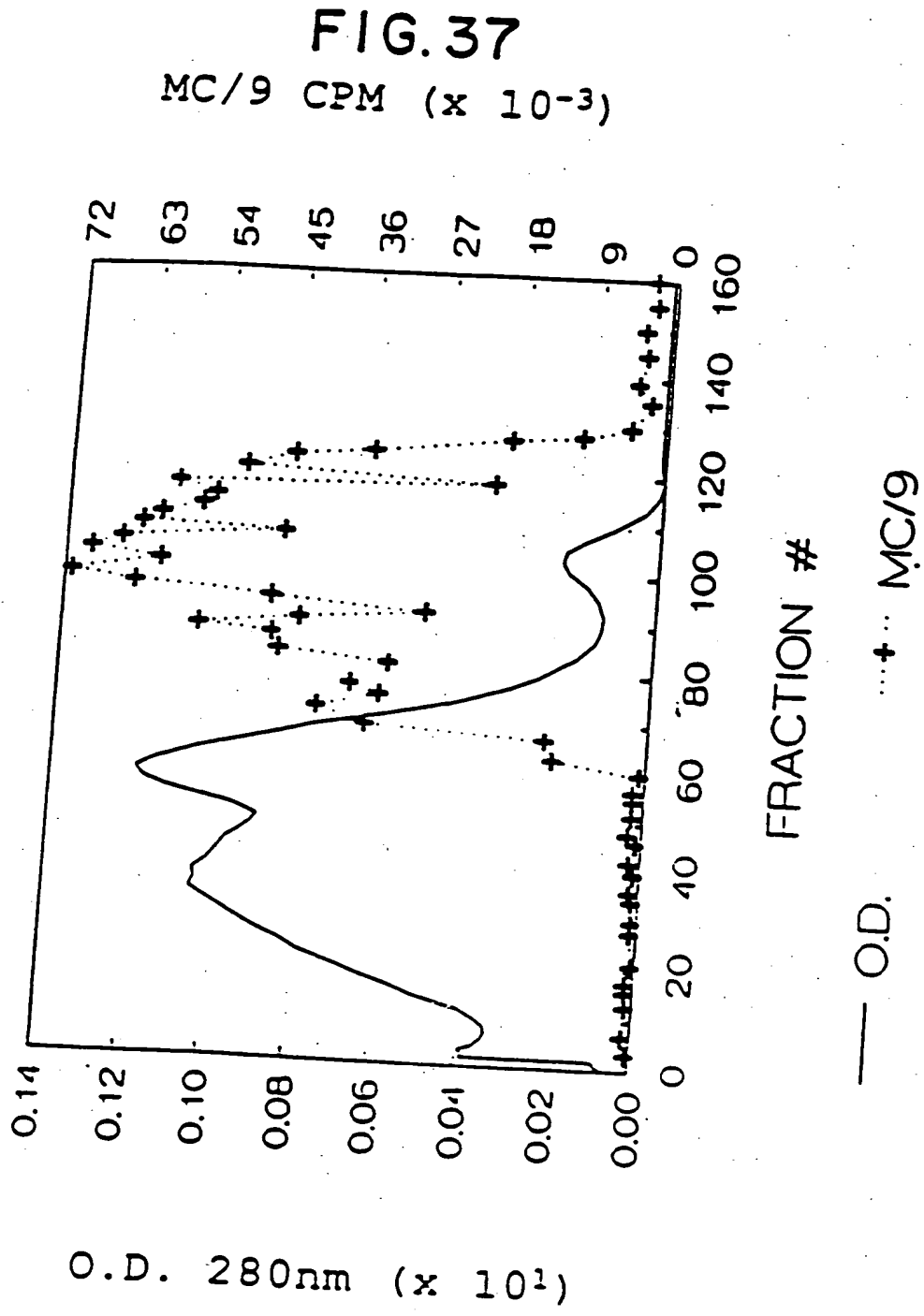


FIG. 38

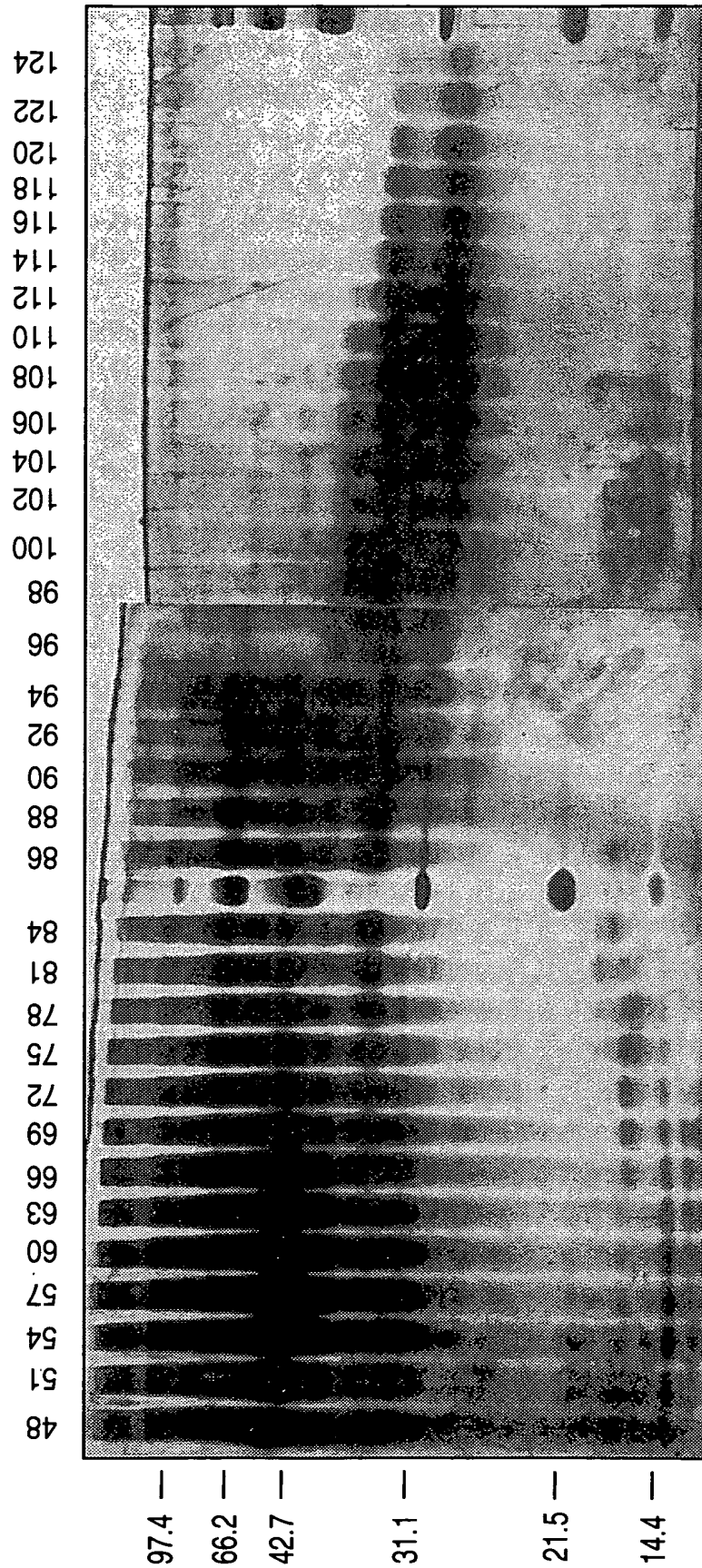


FIG. 39

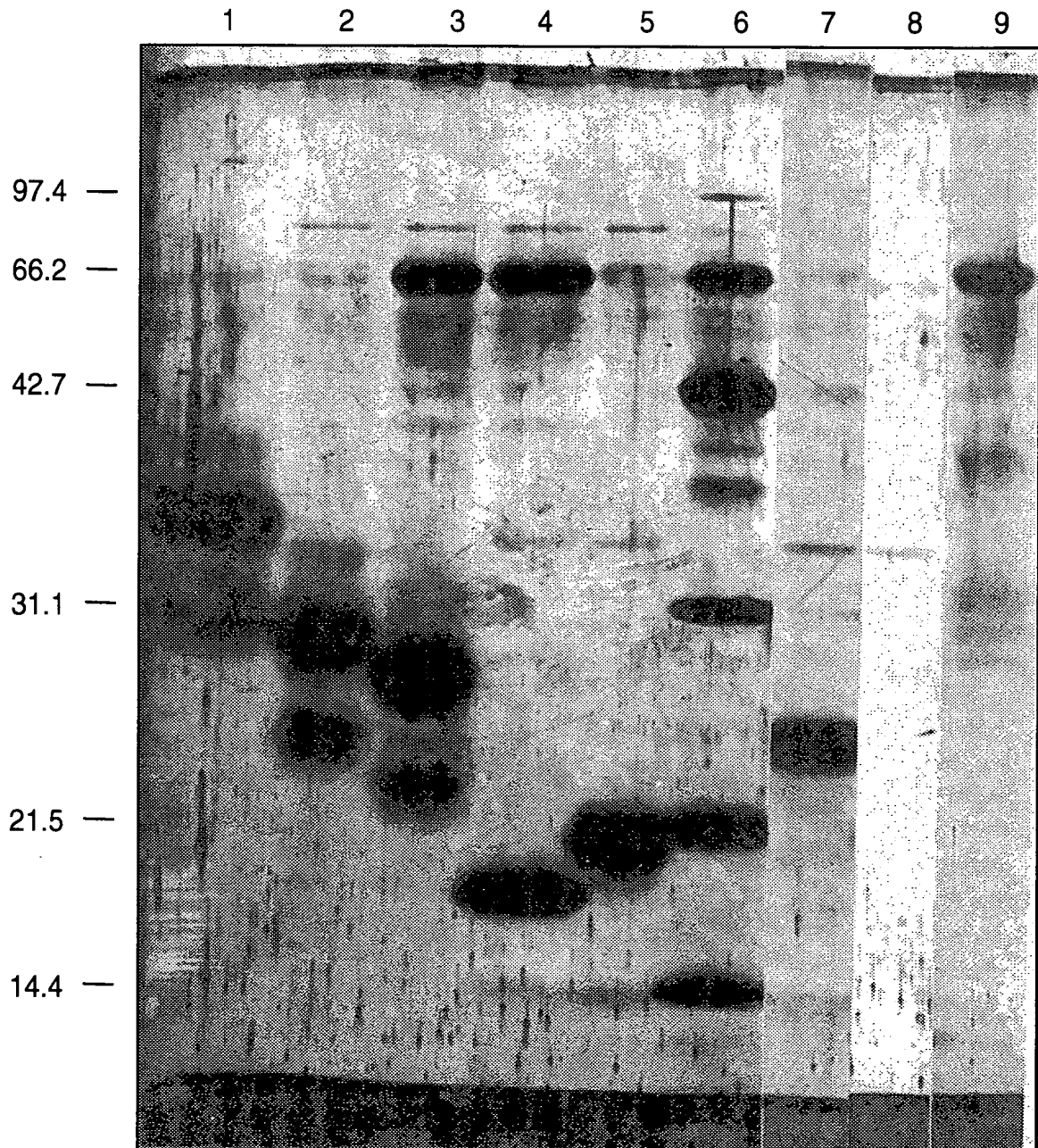


FIG. 40A

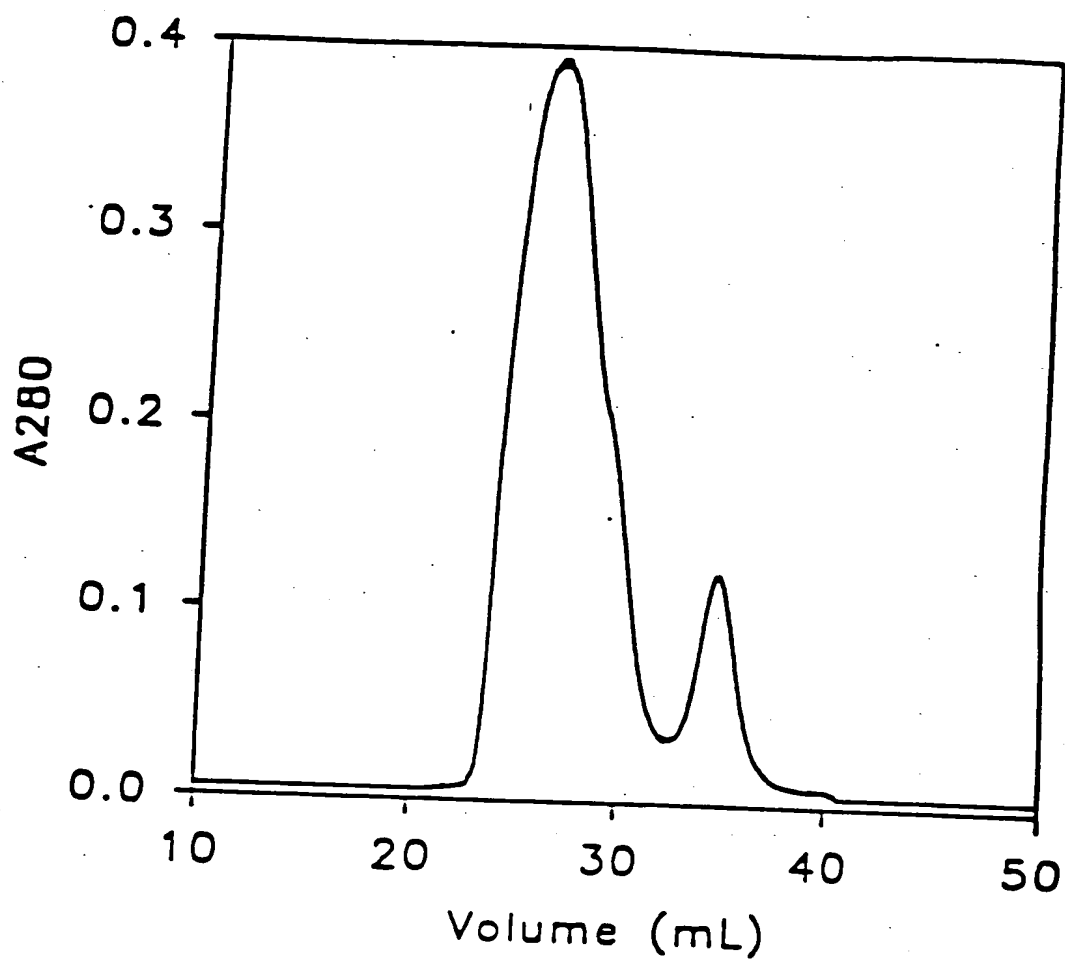


FIG. 40B

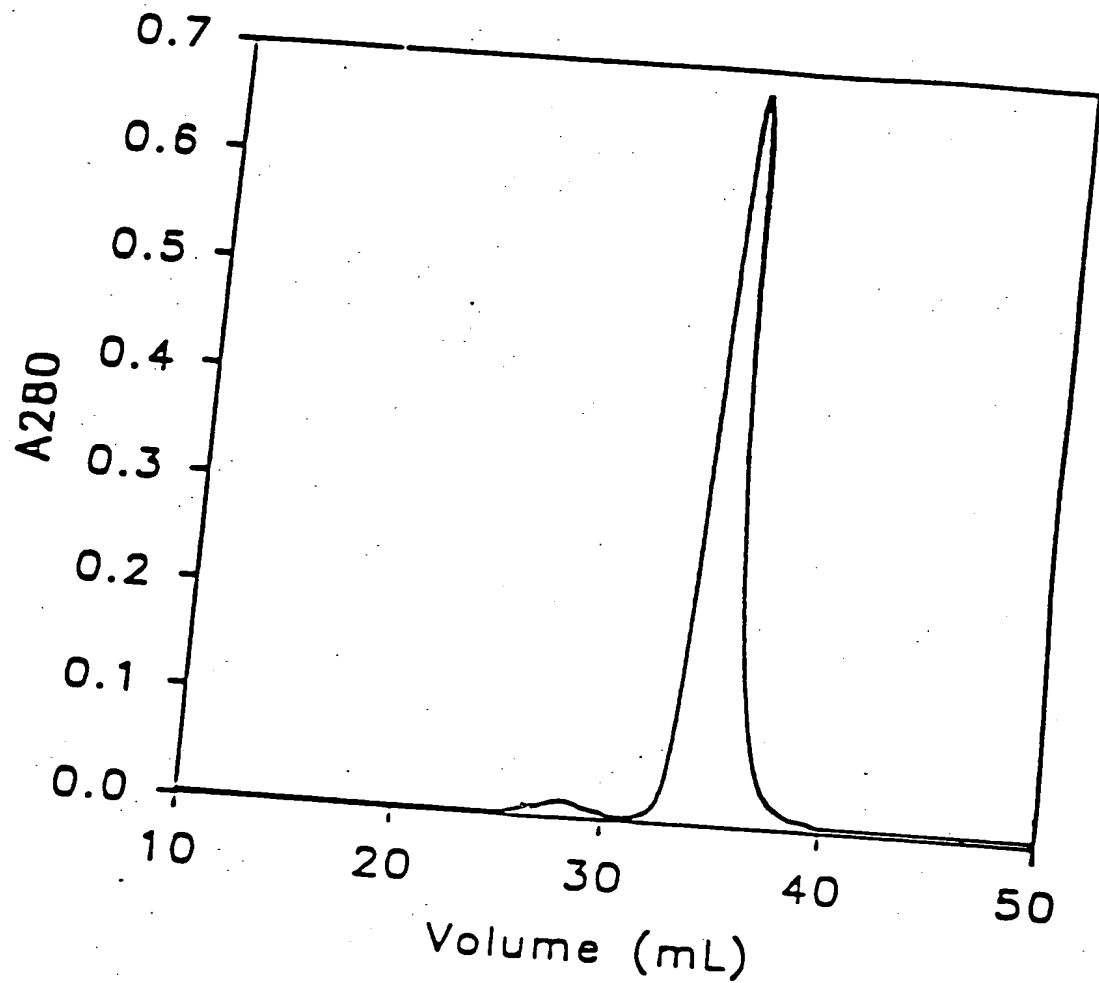


FIG. 41

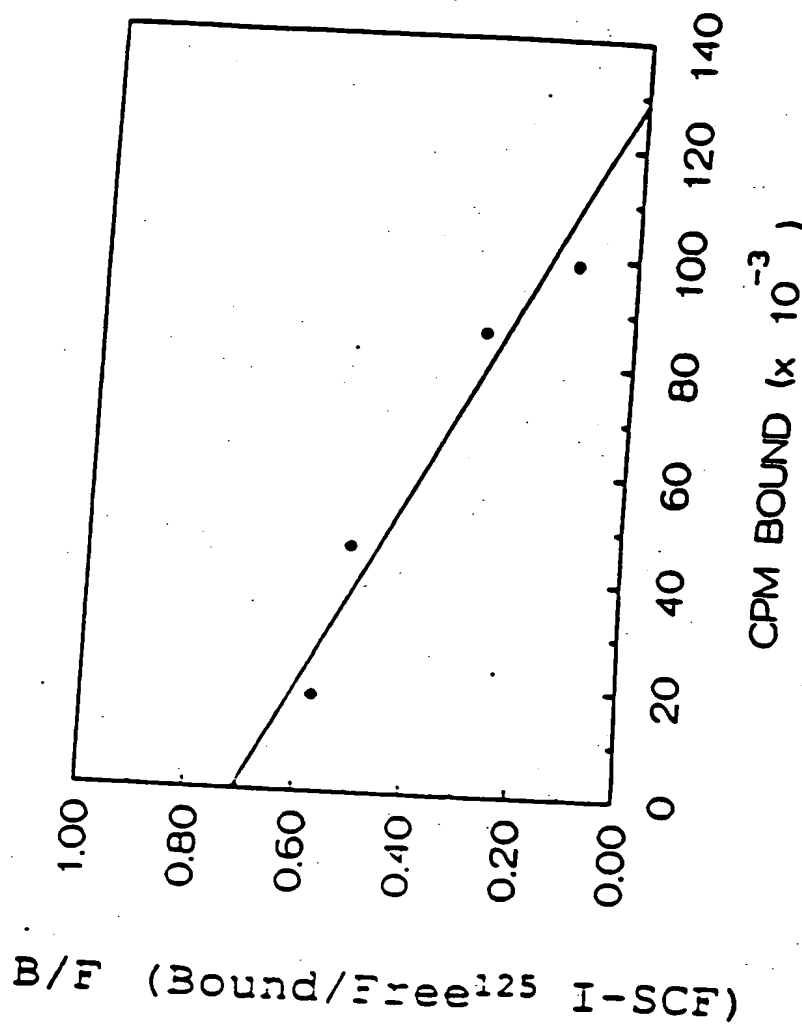


FIG. 42A

CCGCCTCGCGCCGAGACTAGAAAGCGCTGCGGGAAGCAGGACAGTGGAGAGGGCGCTGCGC 61
 TCGGGCTACCCCAATGCGGTGGACTATCTGCCCGCGCTGTTCGTGCAATATGCTGGAGCTCCA 122
 GAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTTCCTT 183
 -25
 Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
 ATG AAG AAG ACA CAA ACT ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 228
 -10
 Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
 CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG 273
 1
 Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala 20
 AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA 318
 10
 Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
 AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG 363
 30
 Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val 50
 ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA 408
 40
 Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
 CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT 453
 60

FIG. 42B

Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG	70	80	498
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT	90	543	
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT	100	110	588
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC	120	633	
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT	130	140	670
Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA	150	723	

FIG. 42C

Lys Pro Phe Met	Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn	170
AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT		768
Asp Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp		180
GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC CCT GGA GAC		813
Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser		190
TCC AGC CTA CAC CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT		858
Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg		210
CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA		903
Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu		220
CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA		948
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe		240
-GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT		993
Gln Glu Val End		248
CAA GAA GTG TAA		
TTGTGGCTTGATCAACACTGTTACTTTCGTACATTGGC		1044

FIG. 42D

TGGTAACAGTTCATGTTTGCTTCATTAATGAAGCAGCTTTAAACAAATTCATATTCTGTC 1104
TGGAGTGACAGACCACATCTTTATCTGTTCTTGCACCCATGACTTTATATGGATGATTC 1164
AGAAATTTGGACAGAAATGTTTTACTGTGAAACTGGCACTGNAATTAATCATCTATAAAGAA 1224
GAACTTGCA TGGAGCAGGACTCTATTTTAAAGGACTGCGGACTTGGGTCTCATTTAGAAC 1284
TTGCAGCTGATGTTGGAAGAGAAAGCAGGTGTCTCAGACTGCATGTACCATTTCATGGC 1344
TCCAGAAATGTCTAAATGCTGMAAAACACCTAGCTTTATTCTTCAGATACAAACTGCAG 1404

FIG. 43

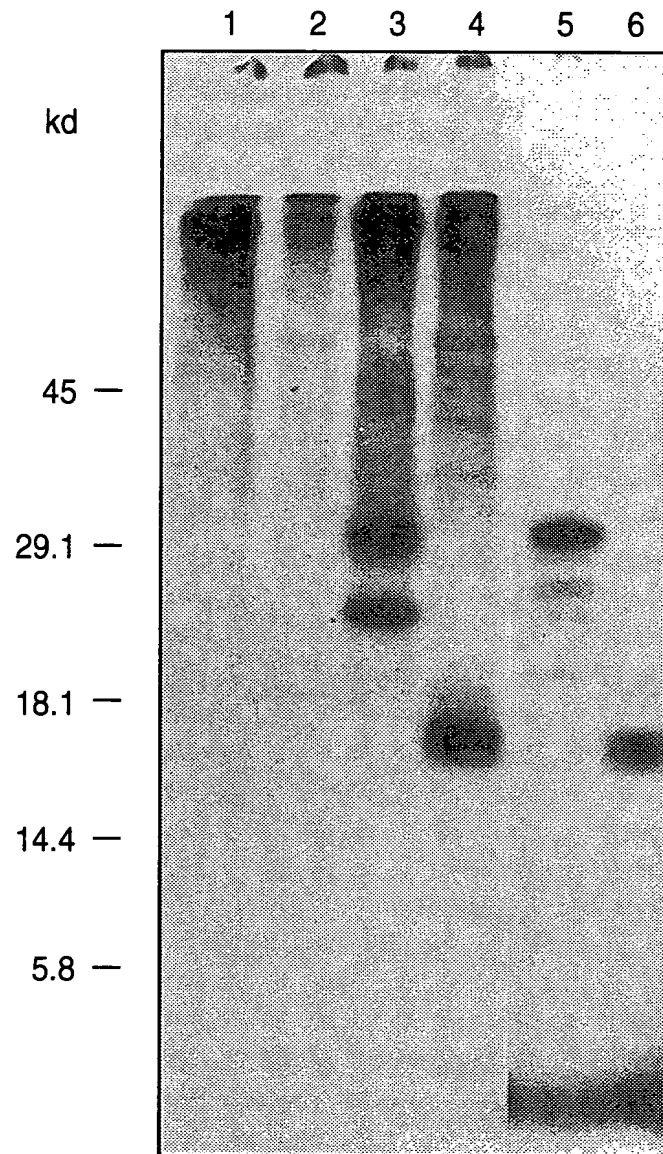


FIG. 44A

AGCAGGGACAGTGGAGAGGGCGCTGCGCTC 30
 GGGCTACCCAAATGCGTGGACTATCTGCCCGCGCTGTTTCGTGCAATATGCTGGAGCTCCAG 90
 AACAGCTAAACGGAGTCGCCACACCACTGTTGTGCTGGATGCGAGCGCTGCCTTTCCTT 150
 -25
 Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
 ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 195
 -10
 Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
 CTG CTC CTA TTT AAT CCT CTC CTC GTC AAA ACT GAA GGG ATC TGC AGG 240
 10
 Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala 20
 AAT CGT GTG ACT AAT AAT GTA NAA GAC GTC ACT AAA TTG GTG GCA 205
 30
 Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
 AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG 330
 40
 Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val 50
 ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA 375

FIG. 44B

Gln	Leu	Ser	Asp	Ser	Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	420
CAA	TTG	TCA	GAC	AGC	TTG	ACT	GAT	CTT	CTG	GAC	AAG	TTT	TCA	AAT	
60															
Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	80
ATT	TCT	GAA	GGC	TTG	AGT	AAT	TAT	TCC	ATC	ATA	GAC	AAA	CTT	GTG	
70															
Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	90
AAT	ATA	GTG	GAT	GAC	CTT	GTG	GAG	TGC	GTG	AAA	GAA	AAC	TCA	TCT	
100															
Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg	Leu	Phe	110
AAG	GAT	CTA	AAA	AAA	TCA	TTC	AAG	AGC	CCA	GAA	CCC	AGG	CTC	TTT	
120															
Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	
ACT	CCT	GAA	GAA	TTC	TTT	AGA	ATT	TTT	AAT	AGA	TCC	ATT	GAT	GCC	600
130															
Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val	140
TTC	AAG	GAC	TTT	GTA	GTG	GCA	TCT	GAA	ACT	AGT	GAT	TGT	GTG	GTT	
150															
Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Gly	Lys	Ala	Lys	Asn	Pro	Pro	
TCT	TCA	ACA	TTA	AGT	CCT	GAG	AAA	GGG	AAG	GCC	AAA	AAT	CCC	CCT	690

FIG. 44C

```

160      Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu      170
      GGA GAC TCC AGC CTA CAC CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG      735

180      Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
      TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG      780

190      Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile
      AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT      825

210      Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg
      AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA      870

220      Glu Phe Gln Glu Val End
      GAG TTT CAA GAA GTG TAA      TTGTGGCTTGTAACAACACTGTTACTTTCGTA      920

      CATTTGGCTGGTAACAGTTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAATTCATA      980
      TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGG      1040

      ATGATTCAGAAATTGGAACAGAAATGTTTTACTGTGAAACTGGCACTGA      1088

```

FIG. 45

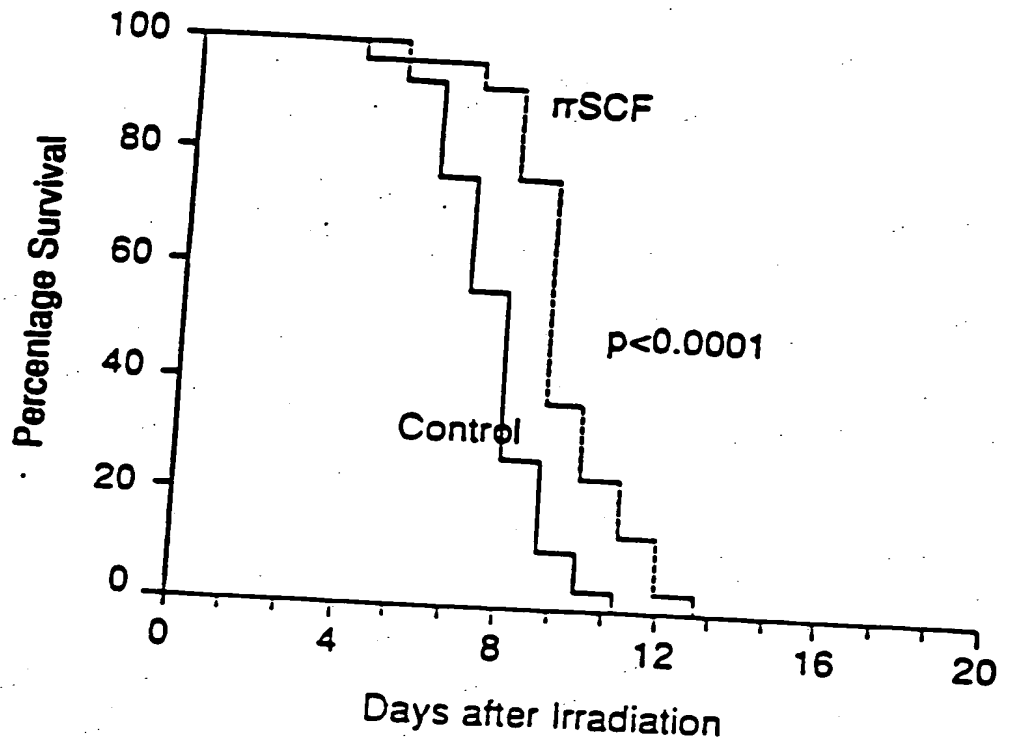


FIG. 46

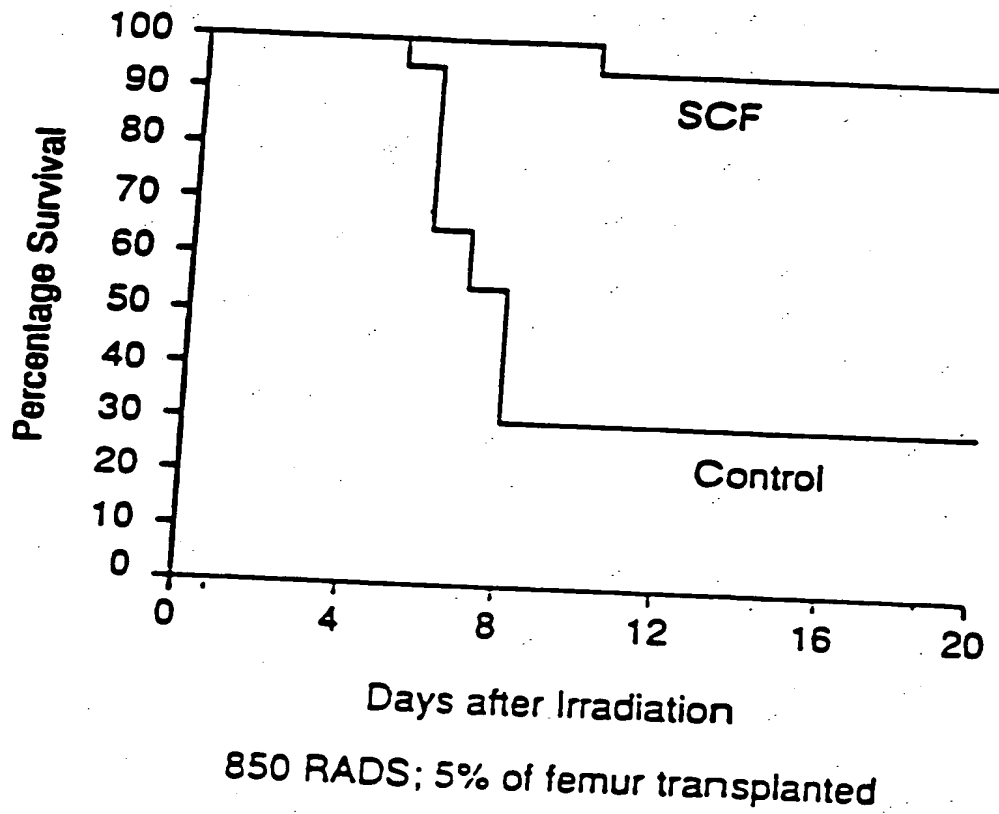


FIG. 47

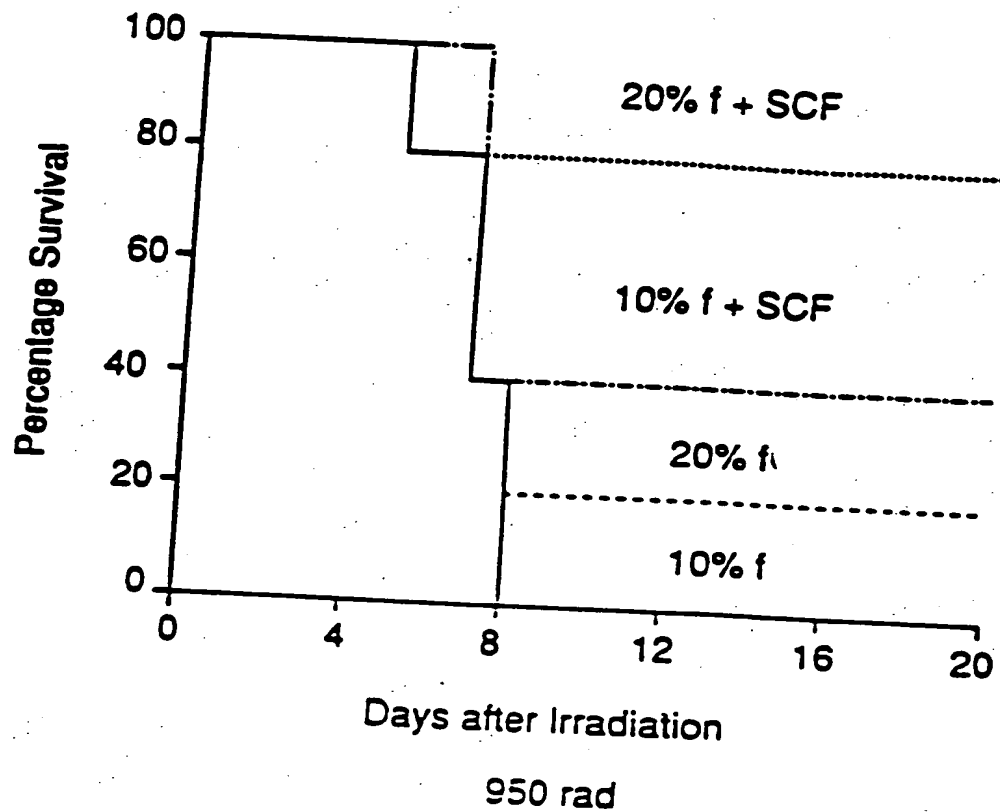


FIG. 48

SCF RADIOPROTECTION (1163 RAD)

Normal Female BDF1 mice, n=30

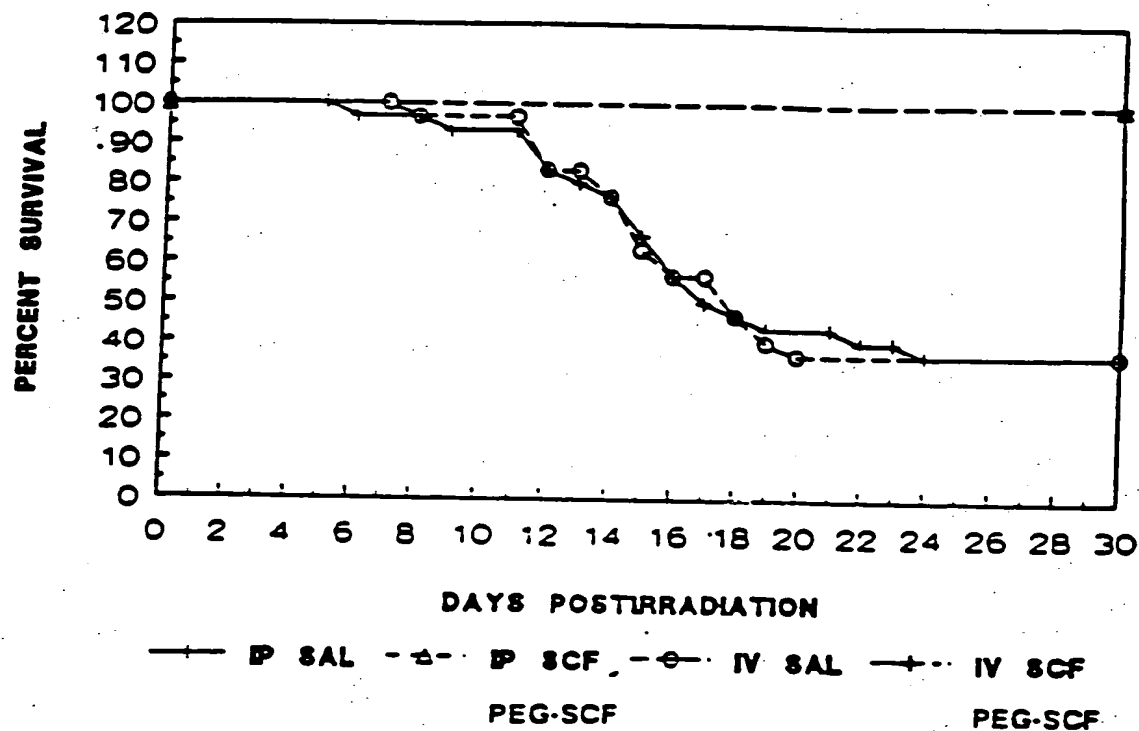


FIG. 49

SCF RADIOPROTECTION (1159 RAD)
Normal Female BDF1 mice

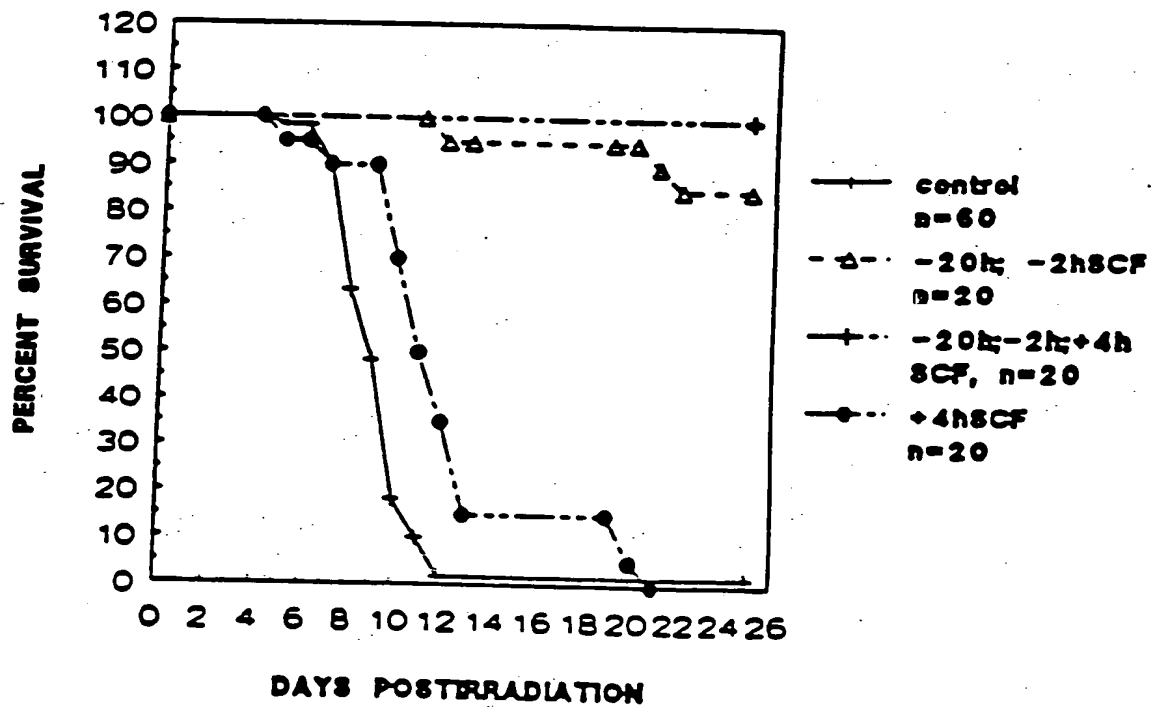


FIG. 50

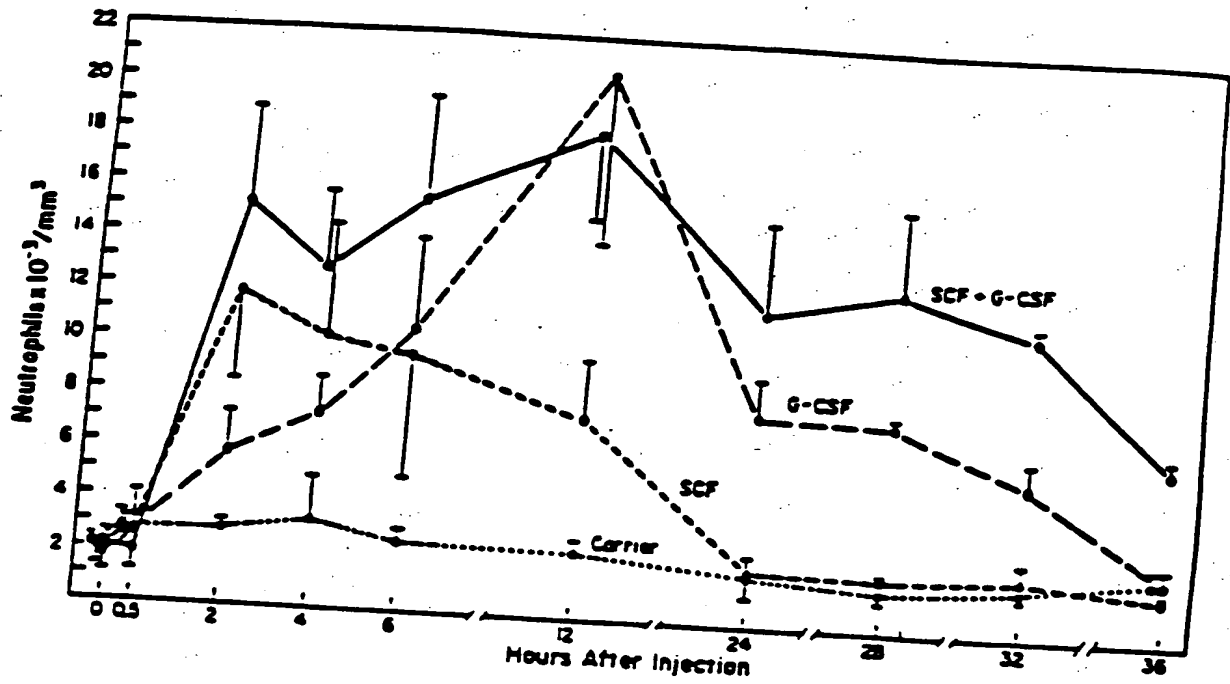


FIG. 51

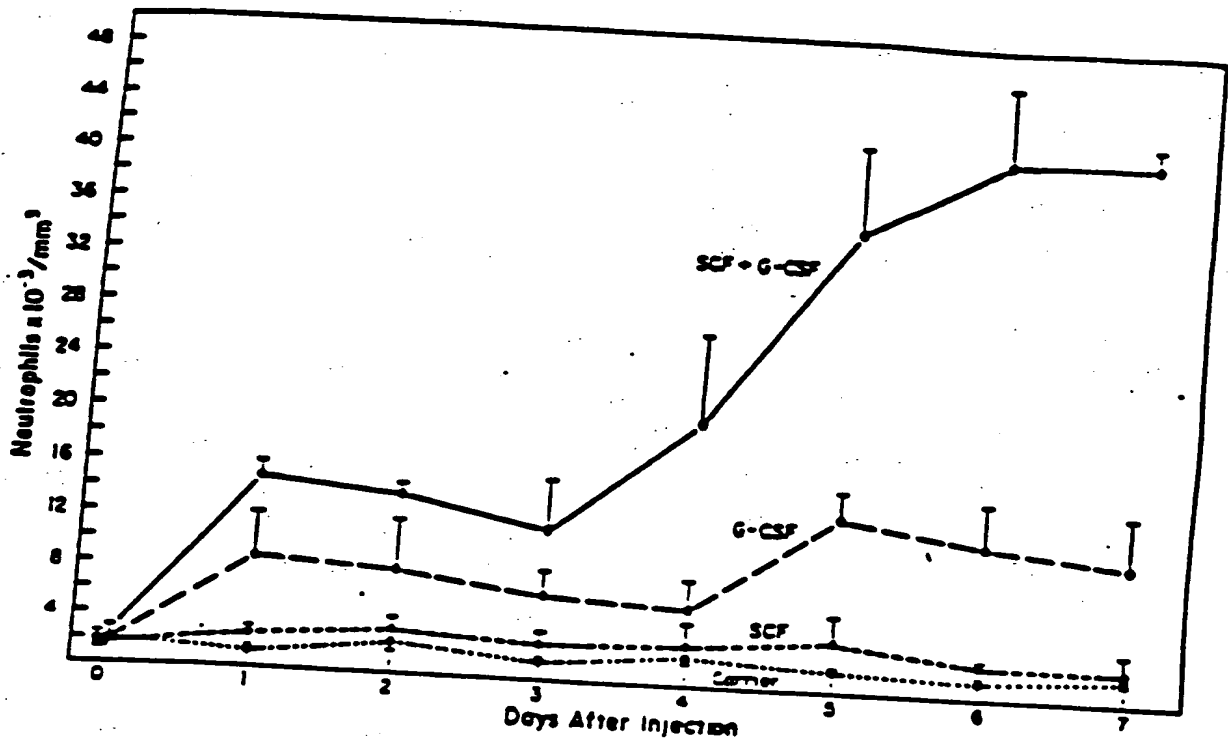


FIG. 52

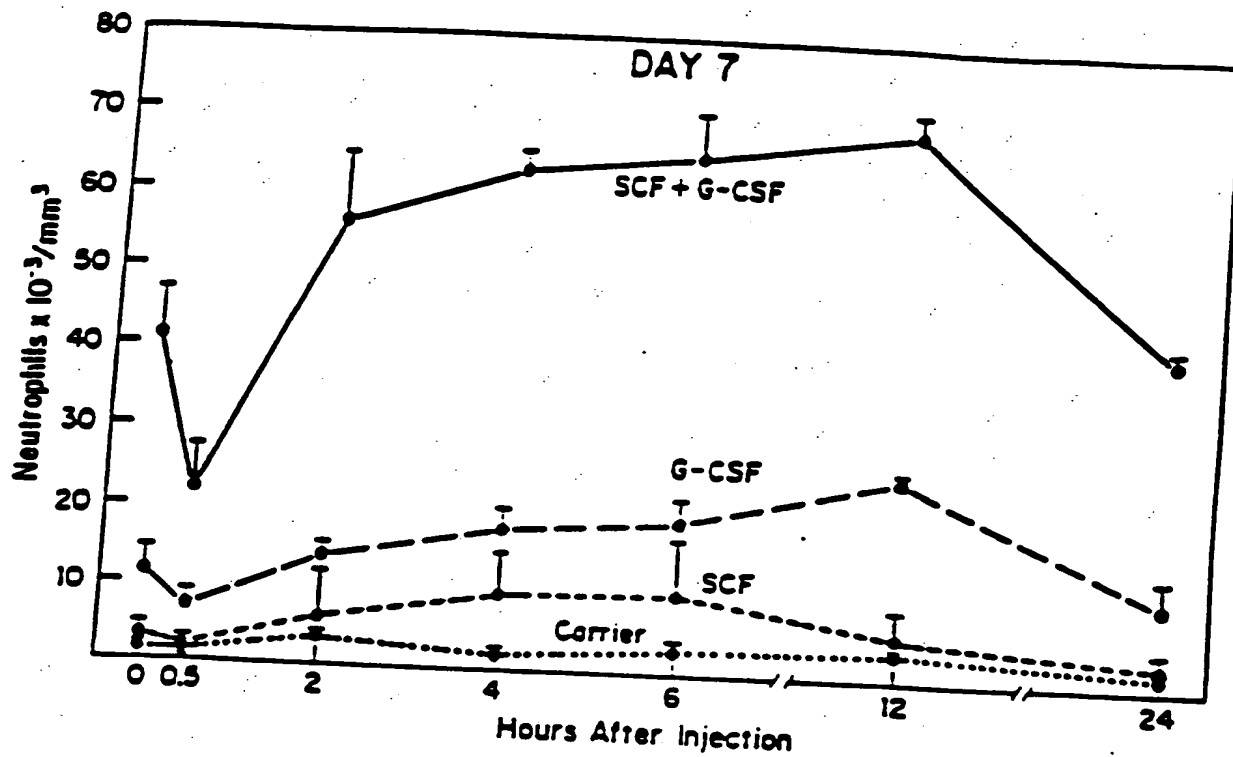


FIG. 53

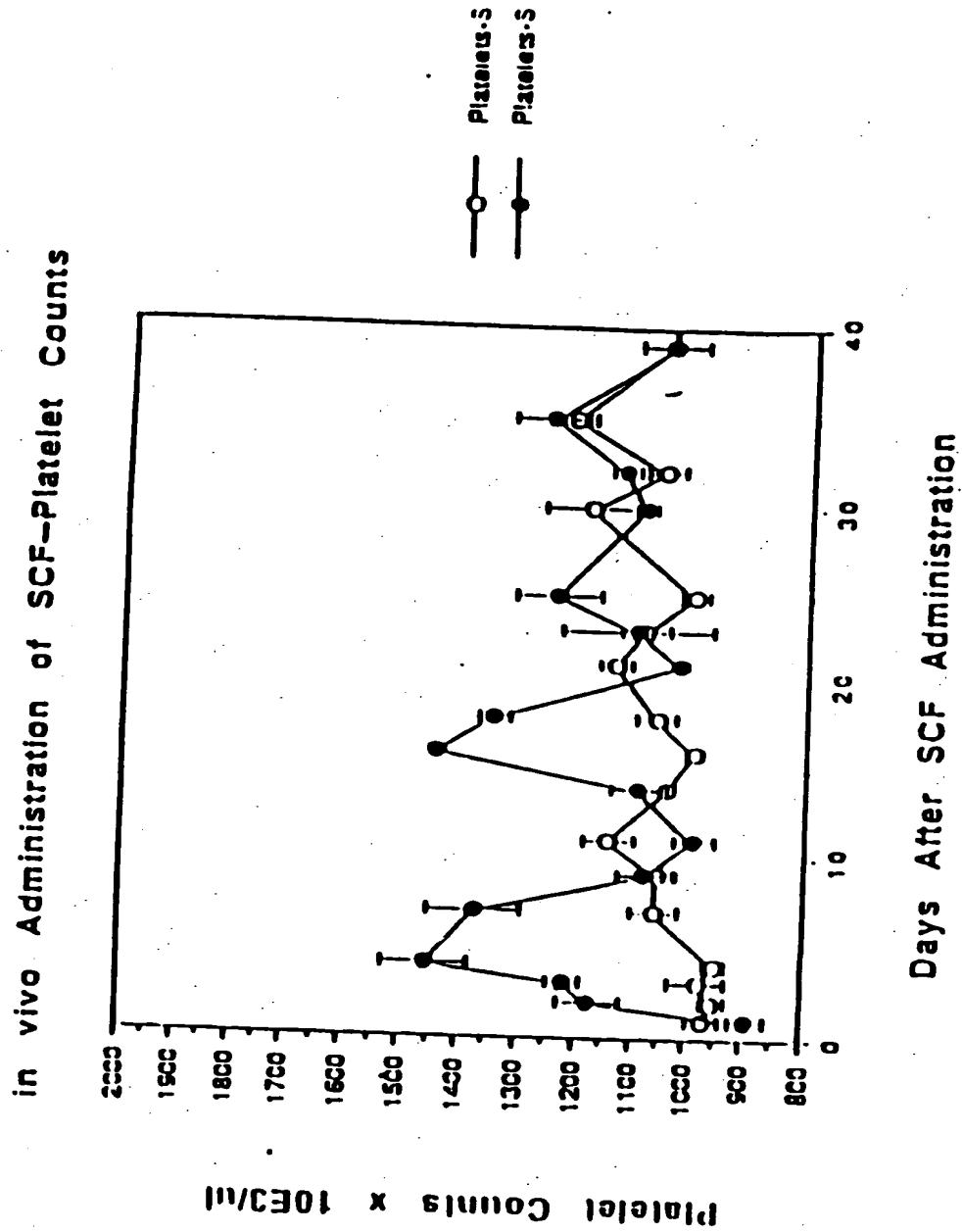


FIG. 54

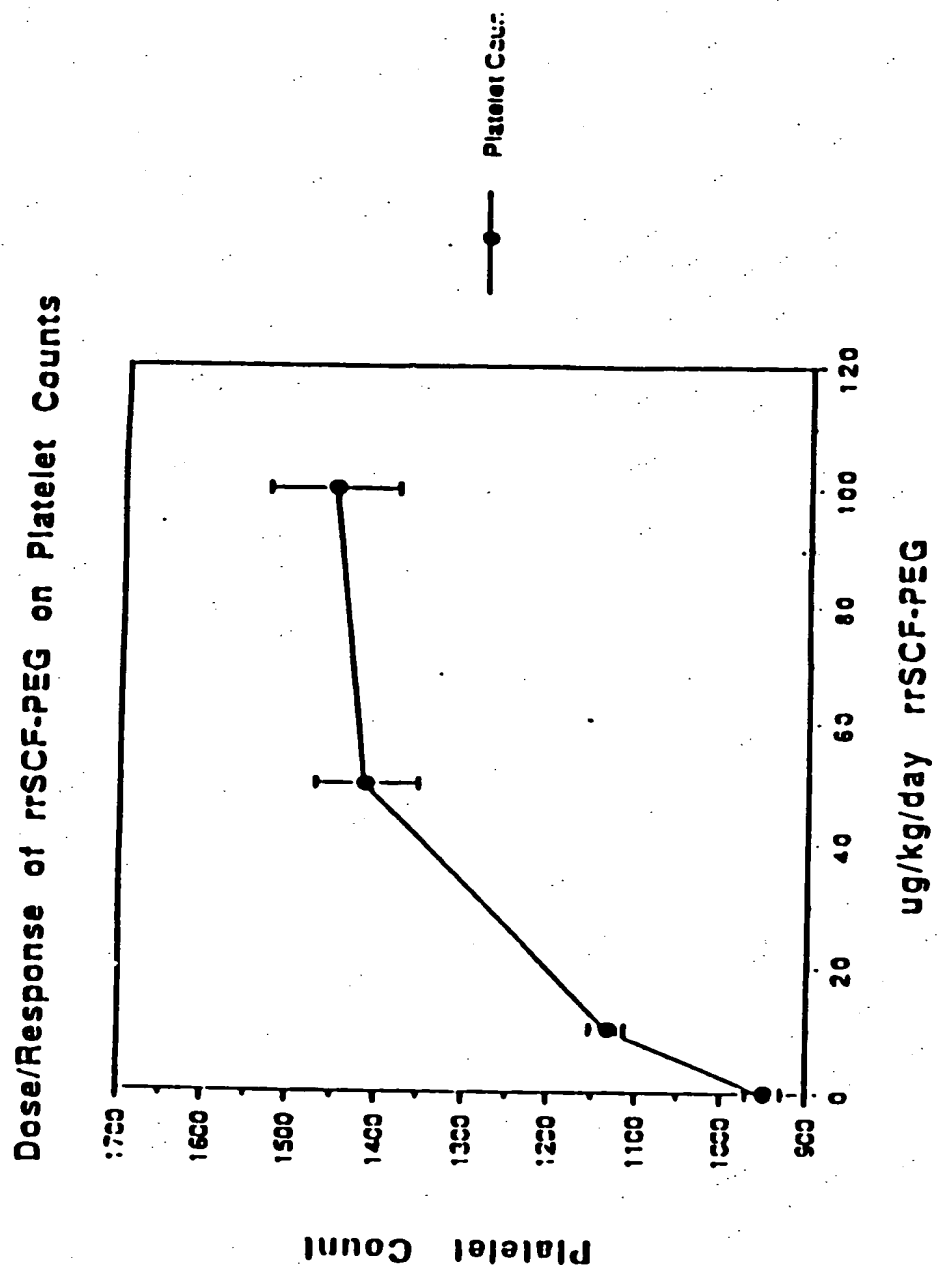


FIG. 55

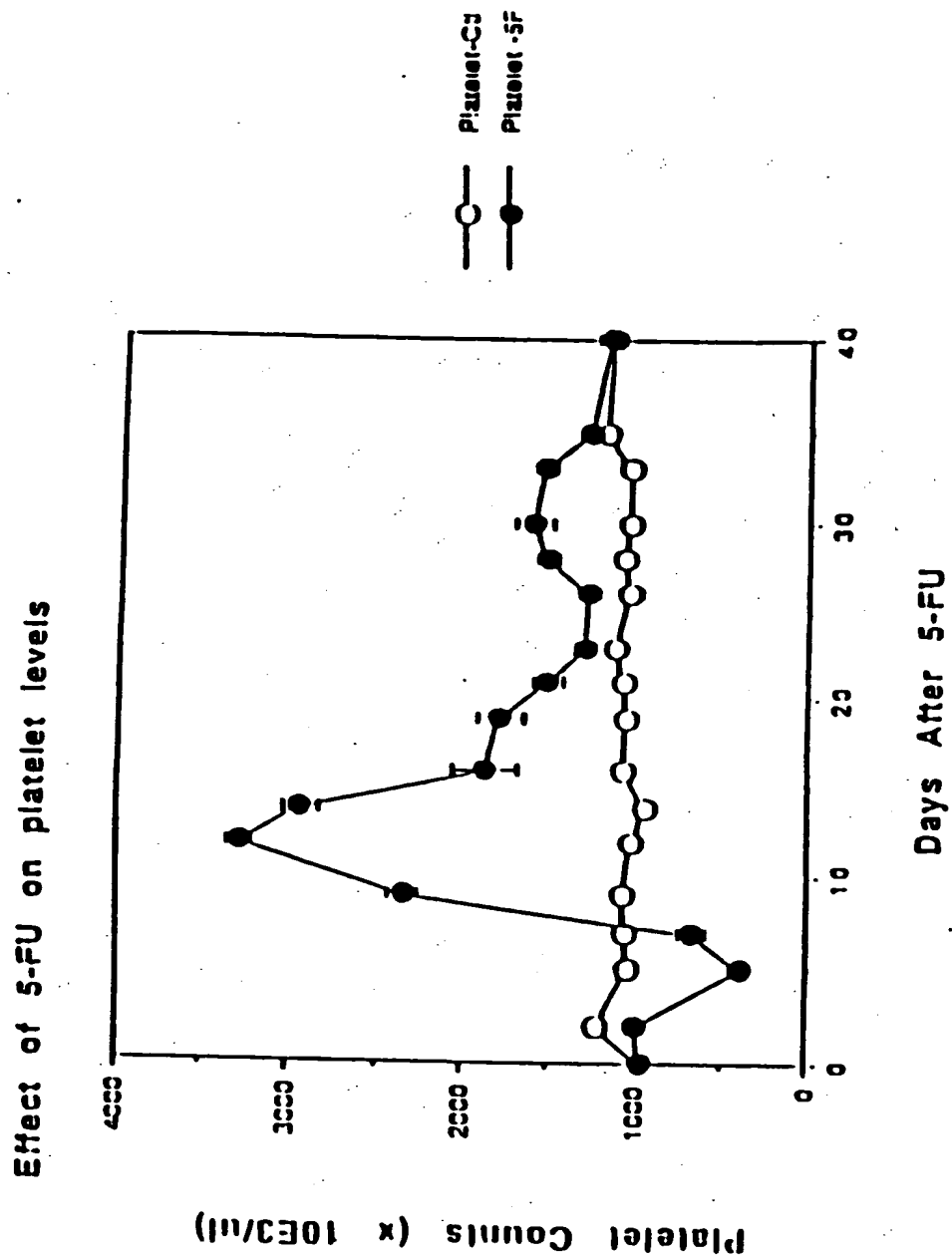
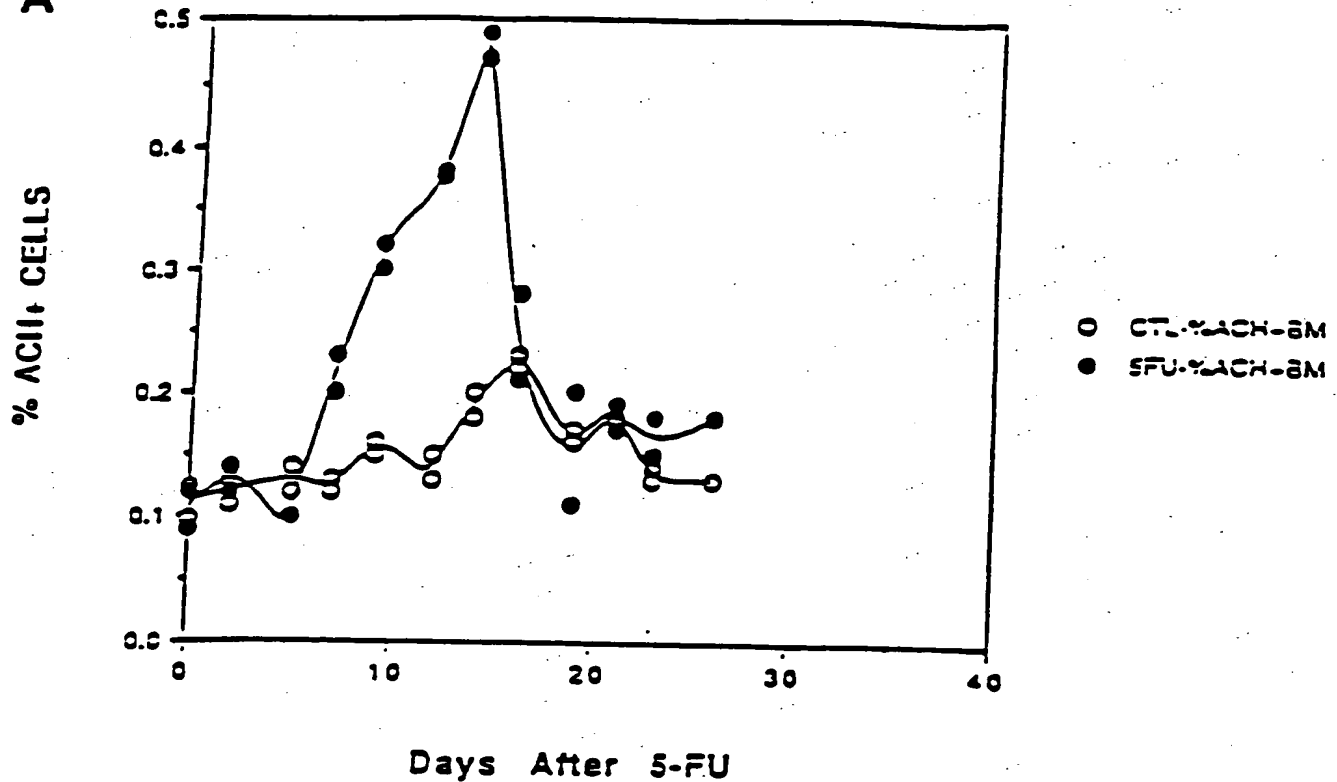


FIG. 56

5-FU Effect on ACH+ Cells in Marrow

A



5-FU Effect on ACH+ Cells in Spleen

B

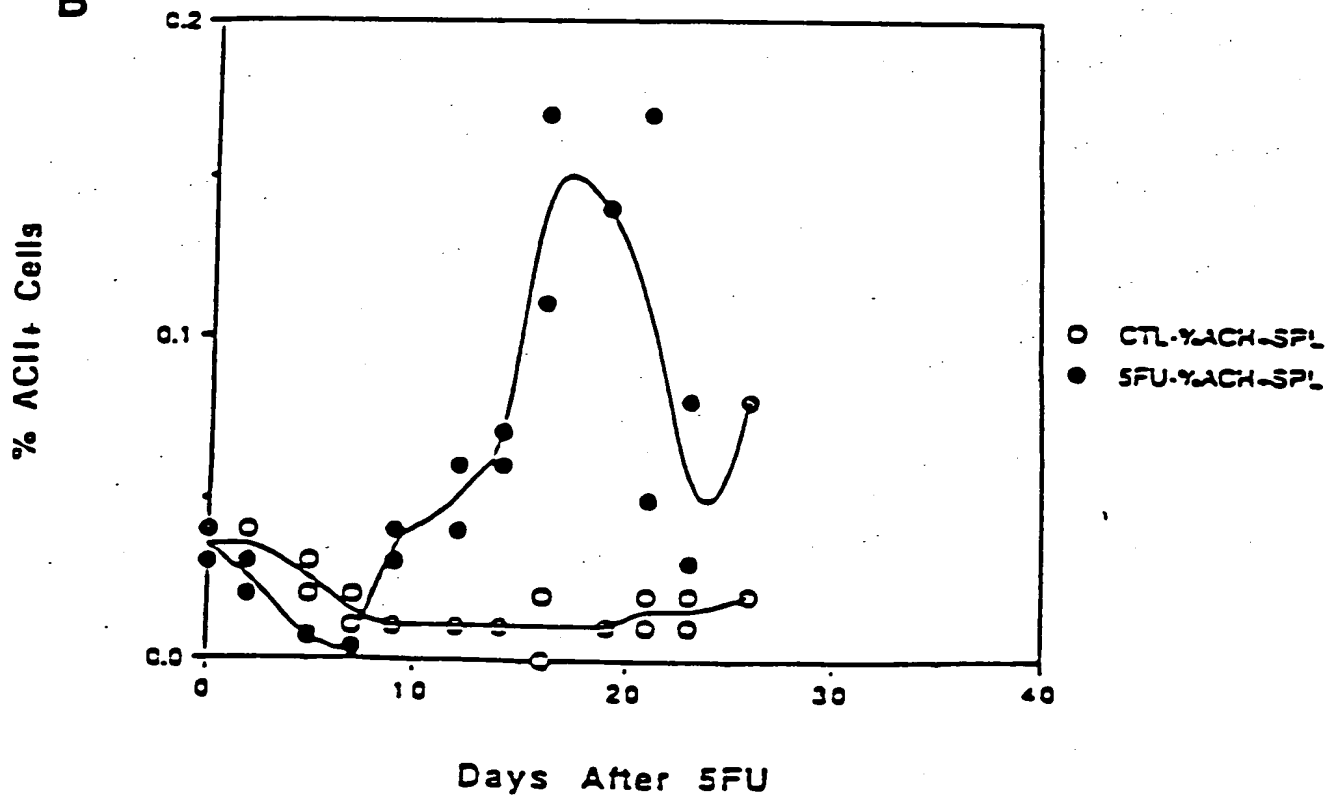


FIG. 57

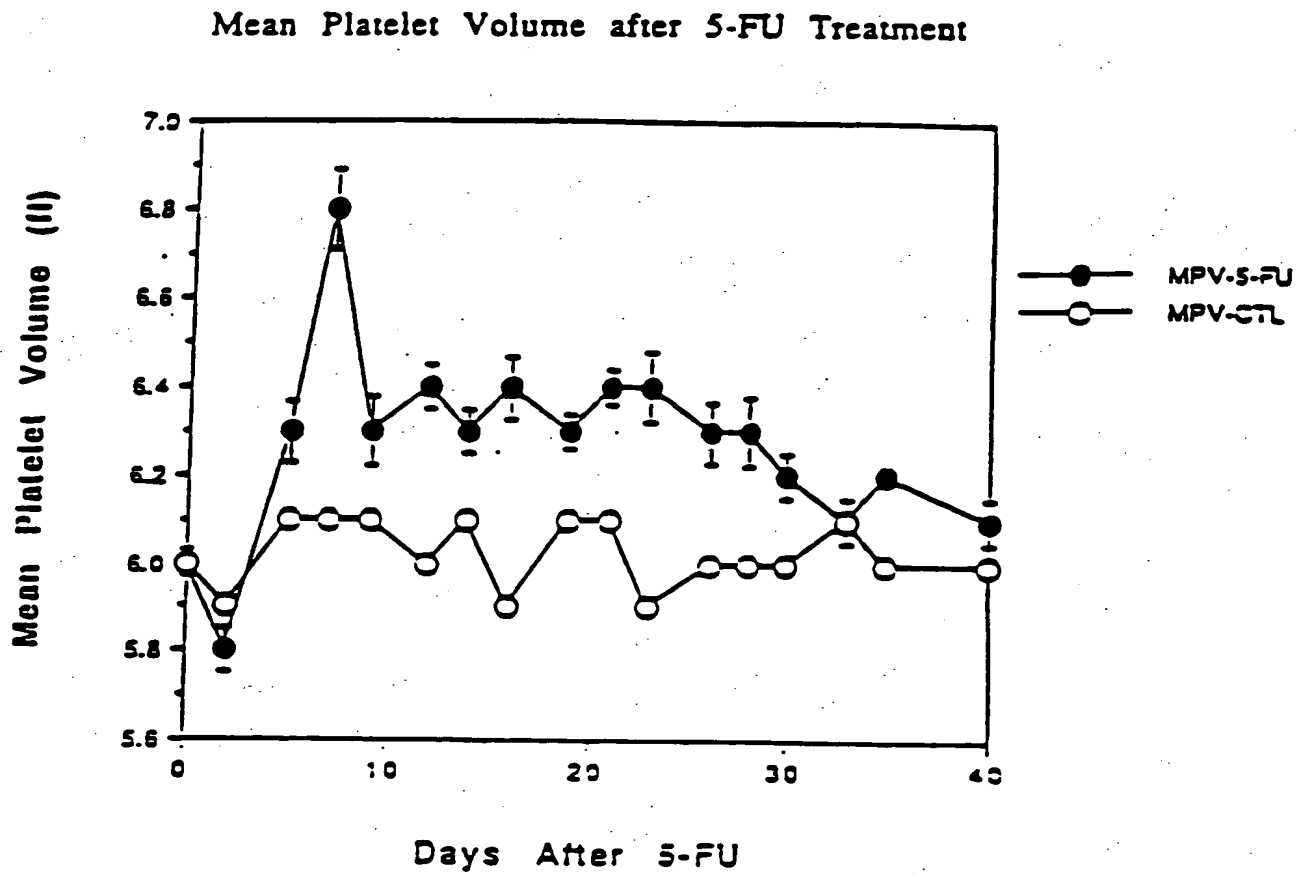


FIG. 58

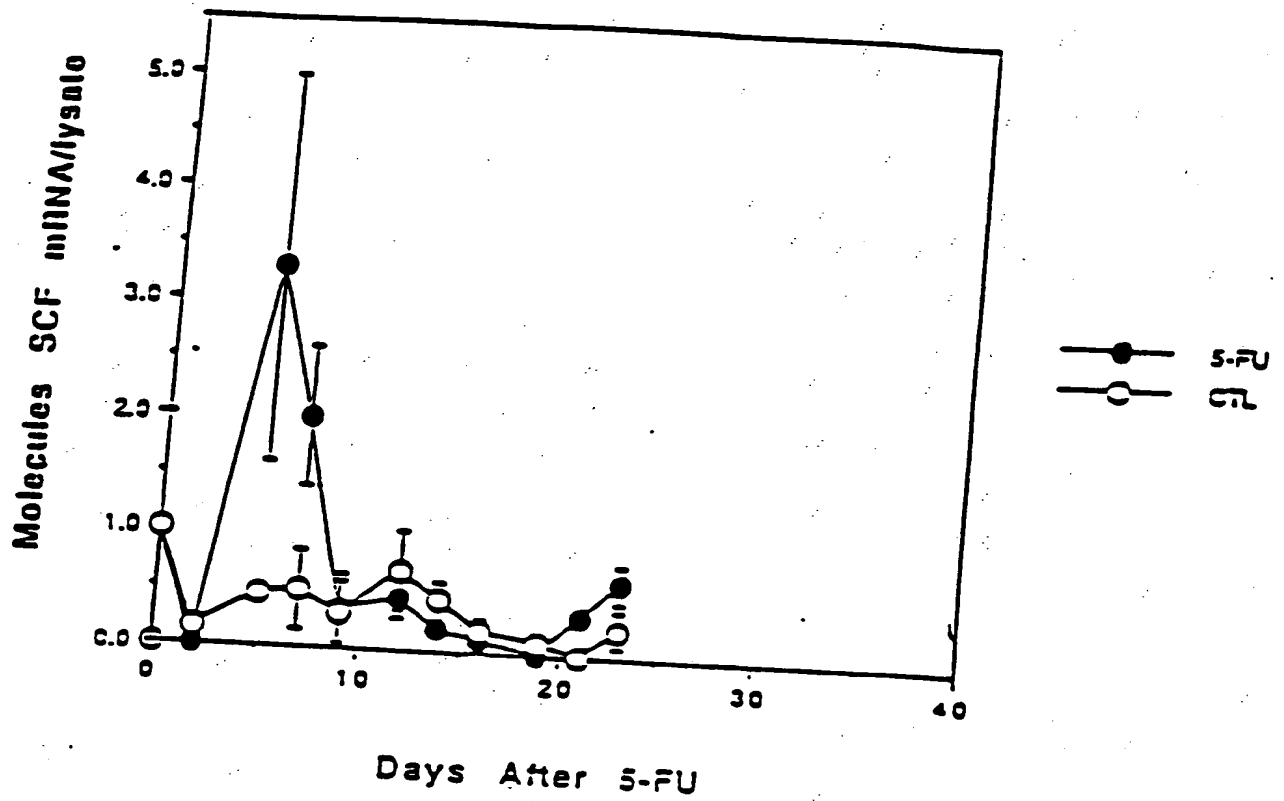


FIG. 59

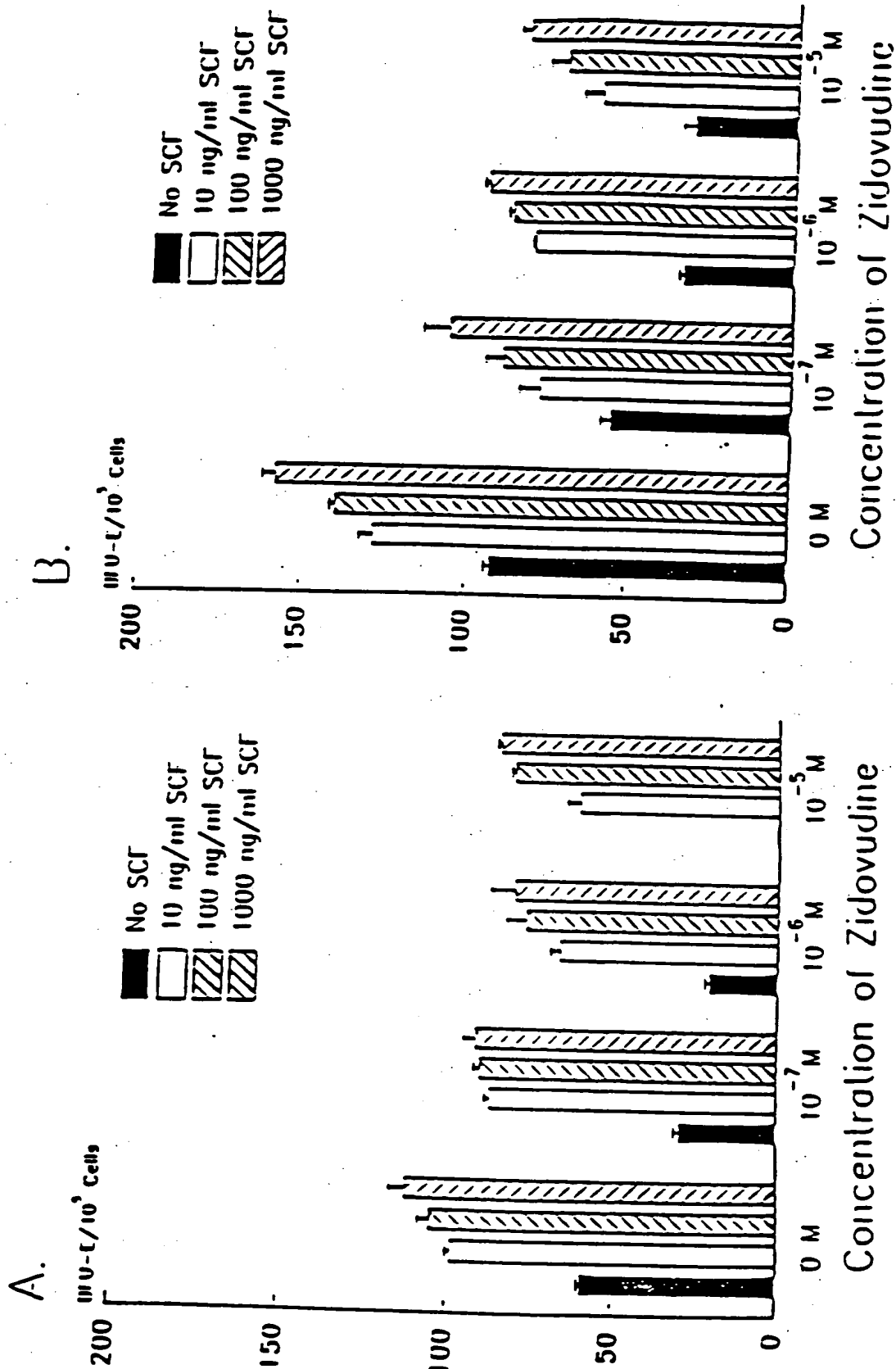


FIG. 60

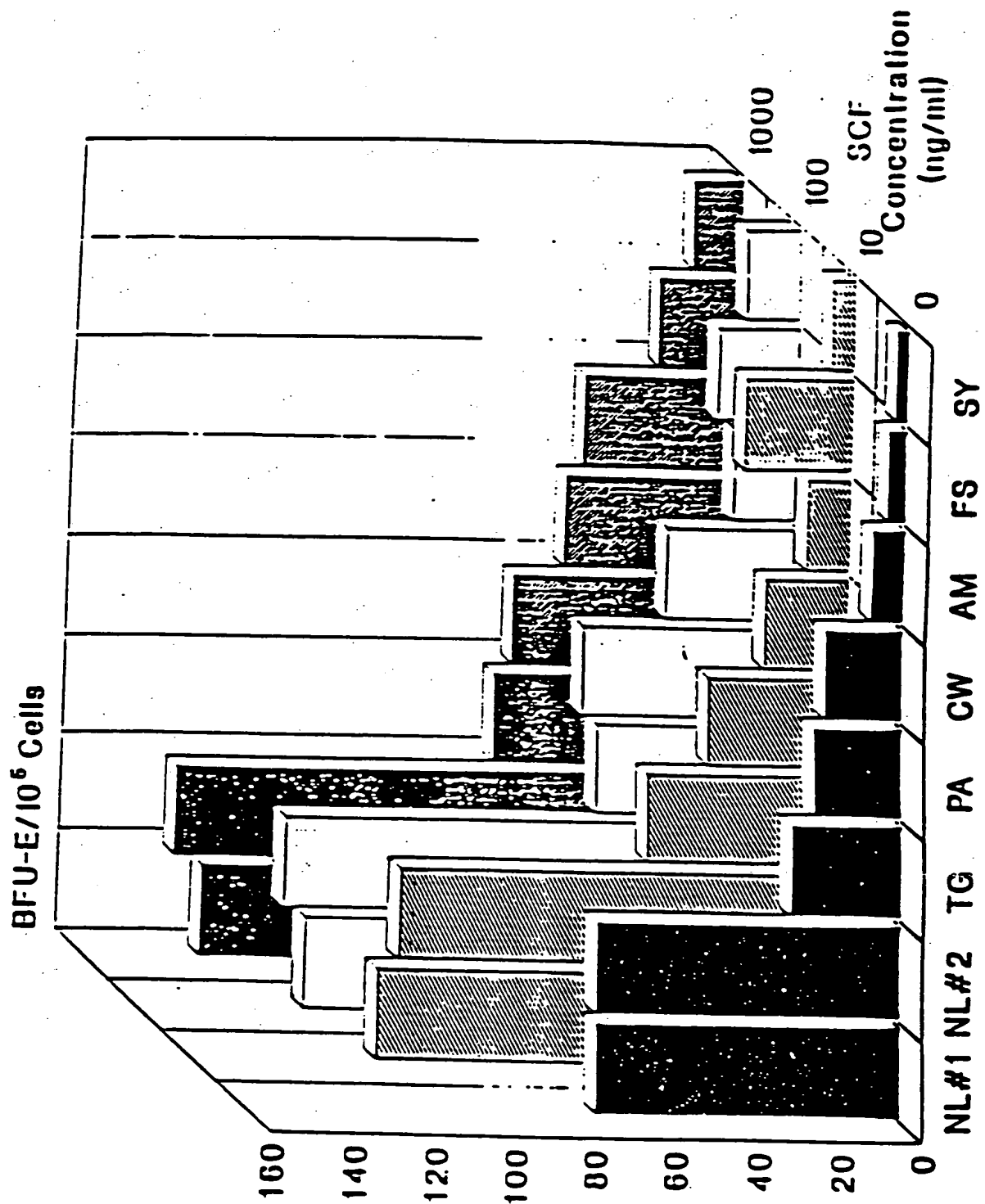


FIG. 61

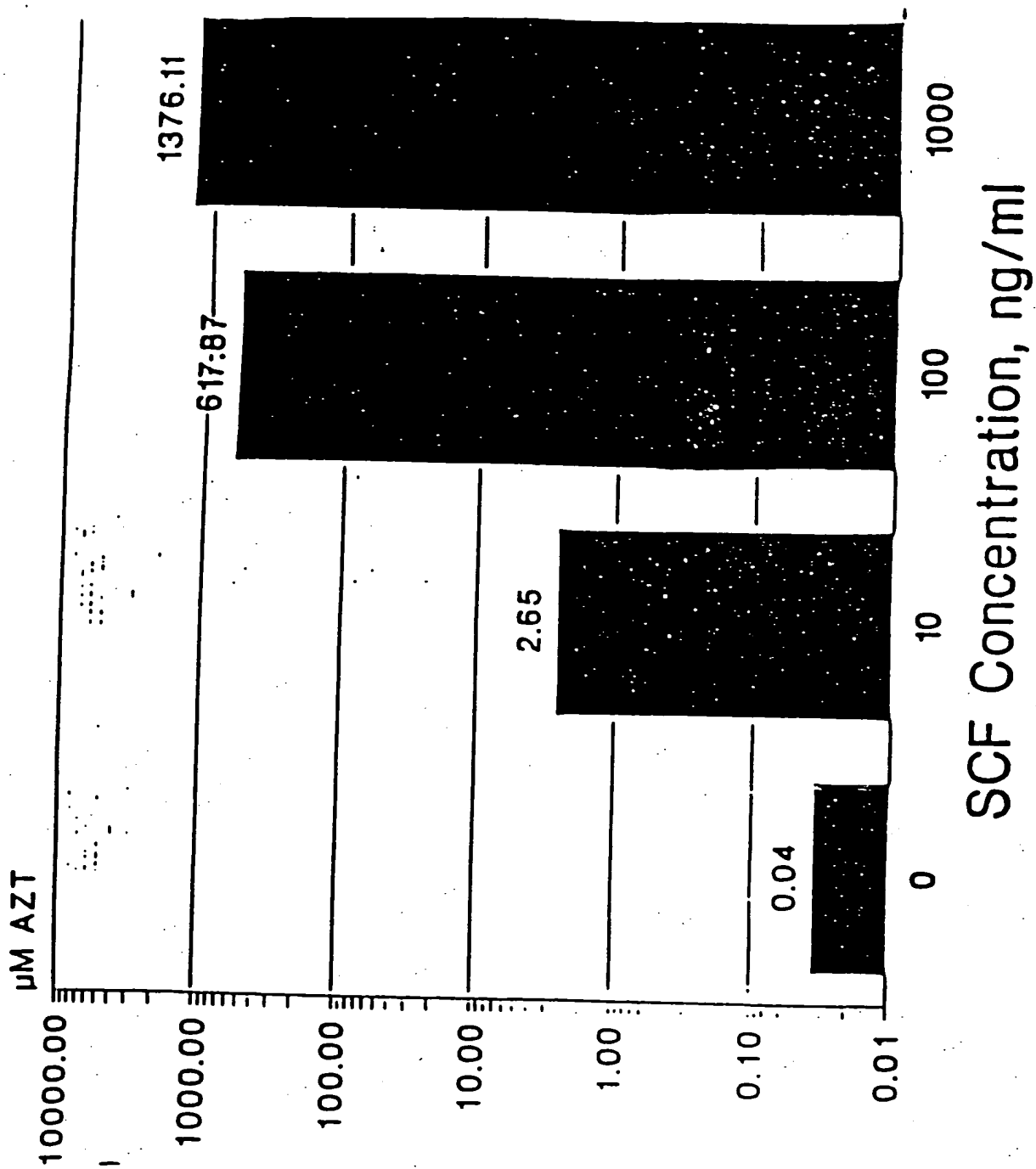


FIG. 62

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

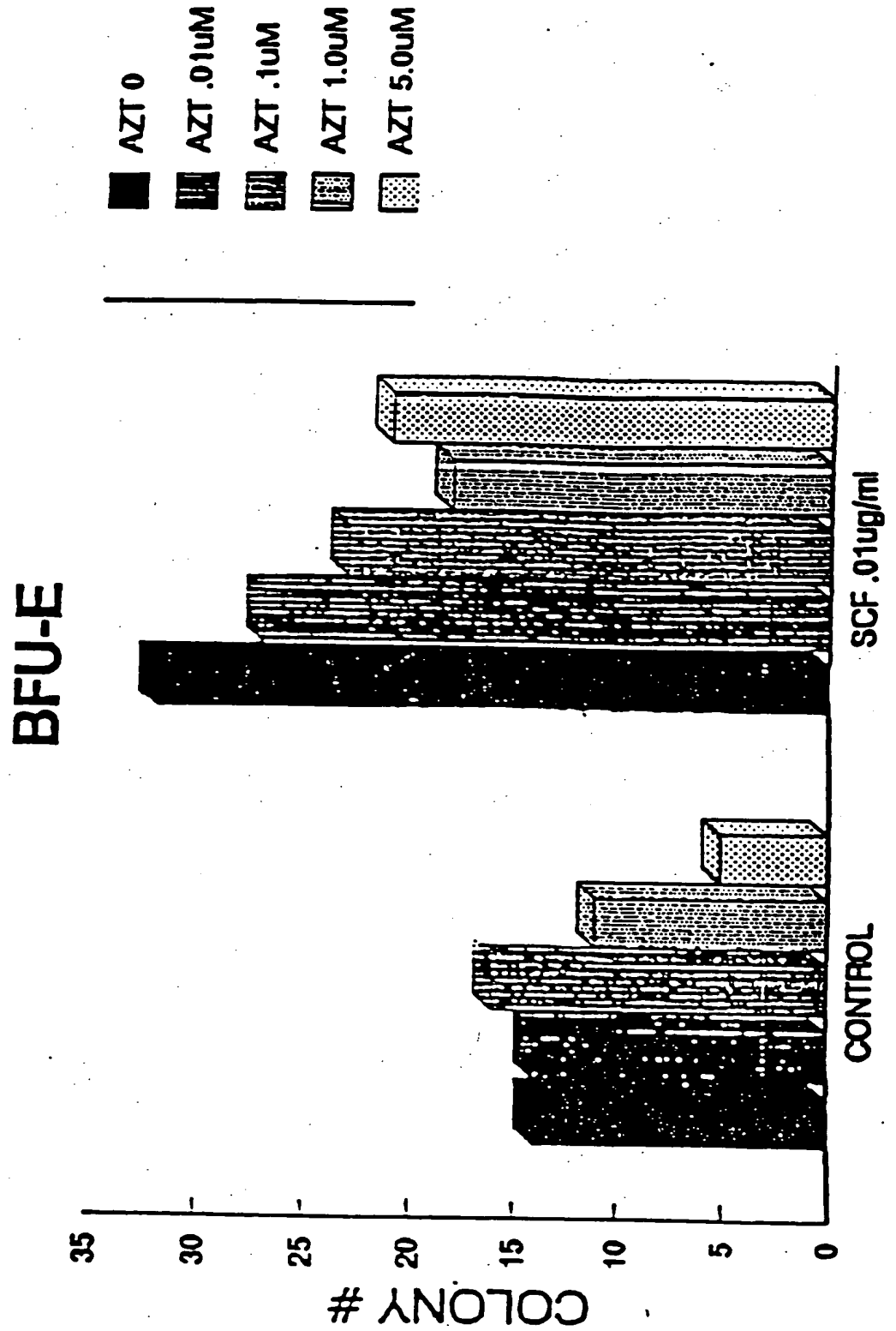


FIG. 63

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

CFU-GM

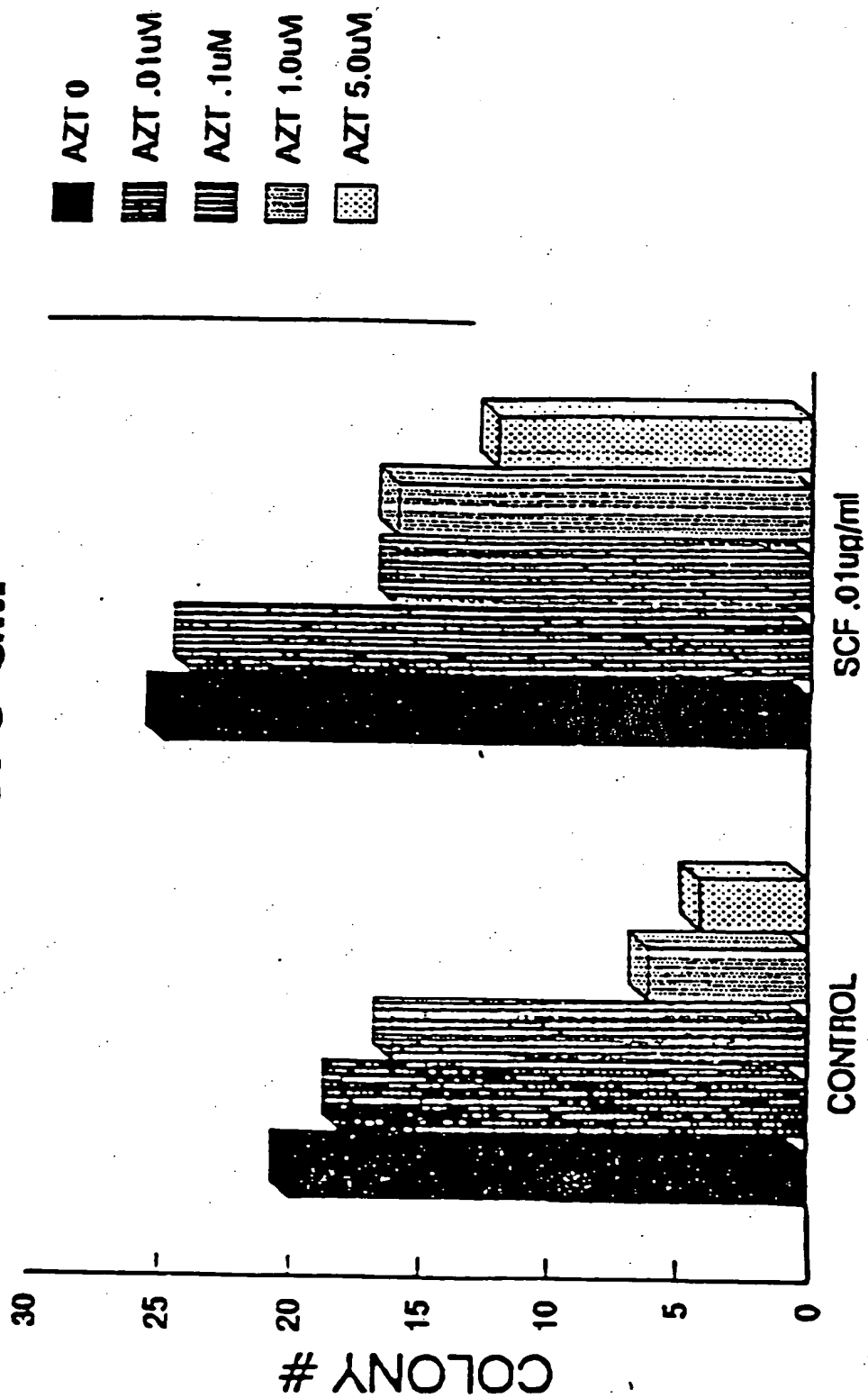


FIG. 64

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

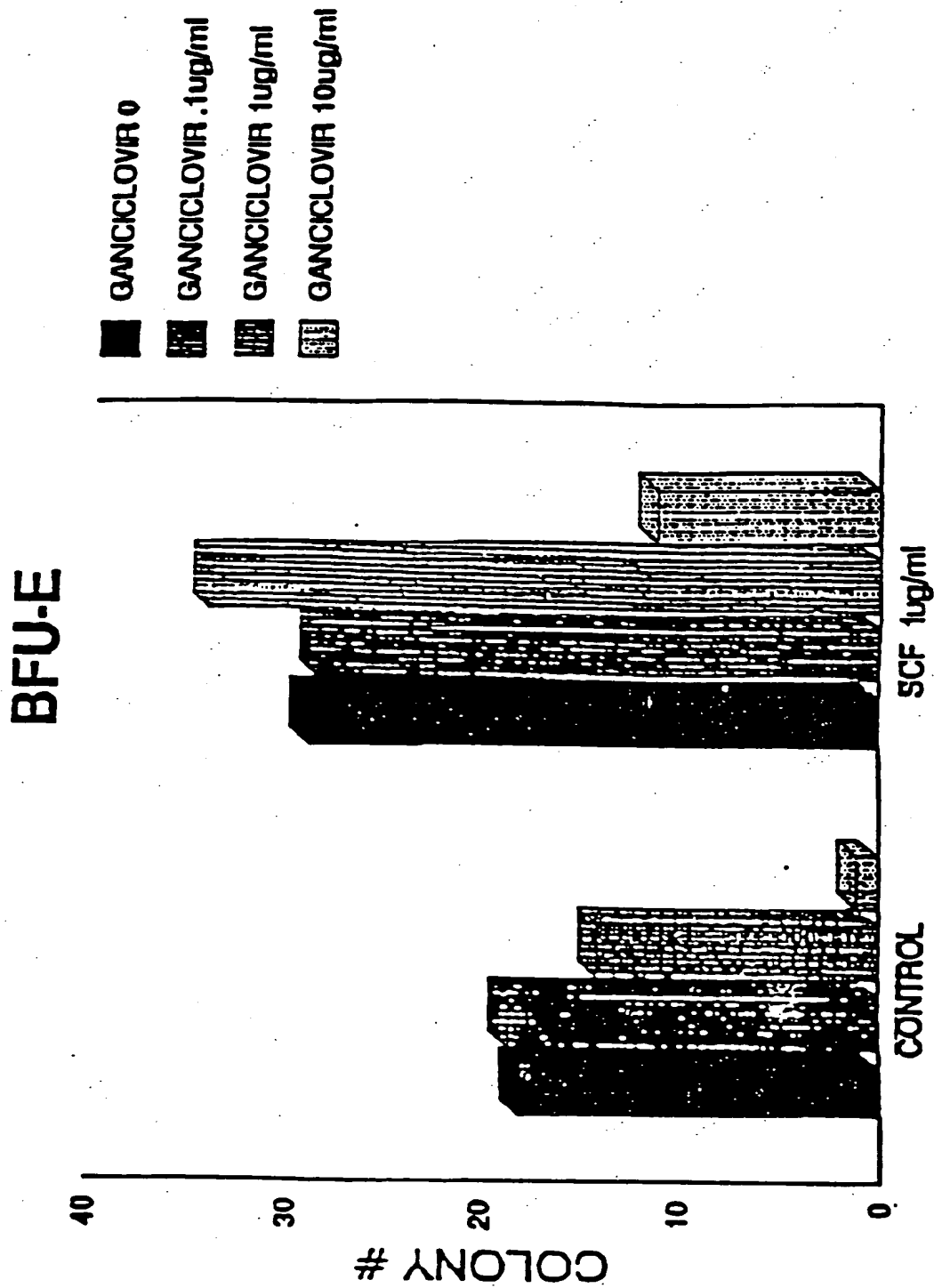


FIG. 65

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

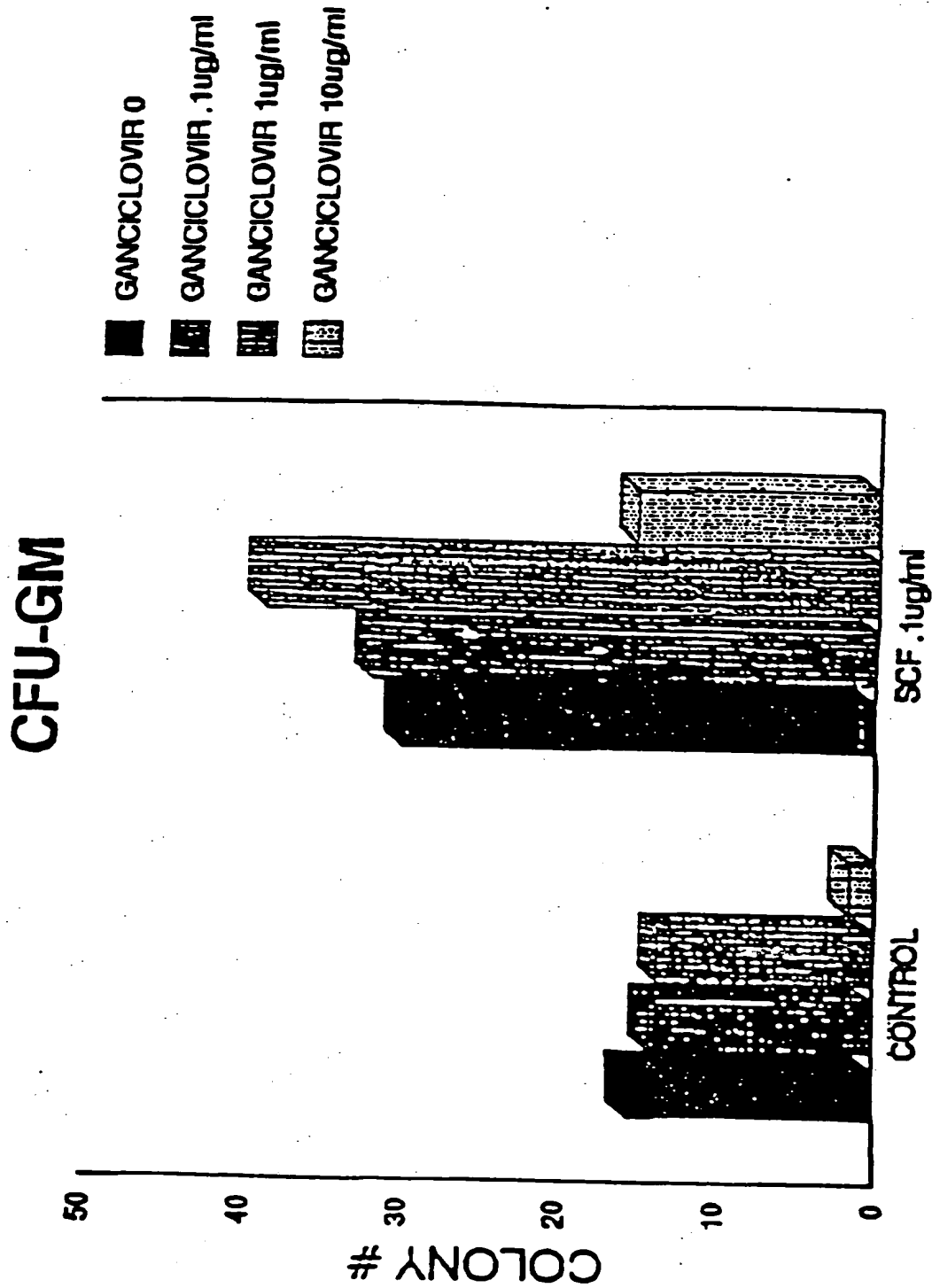


FIG. 66

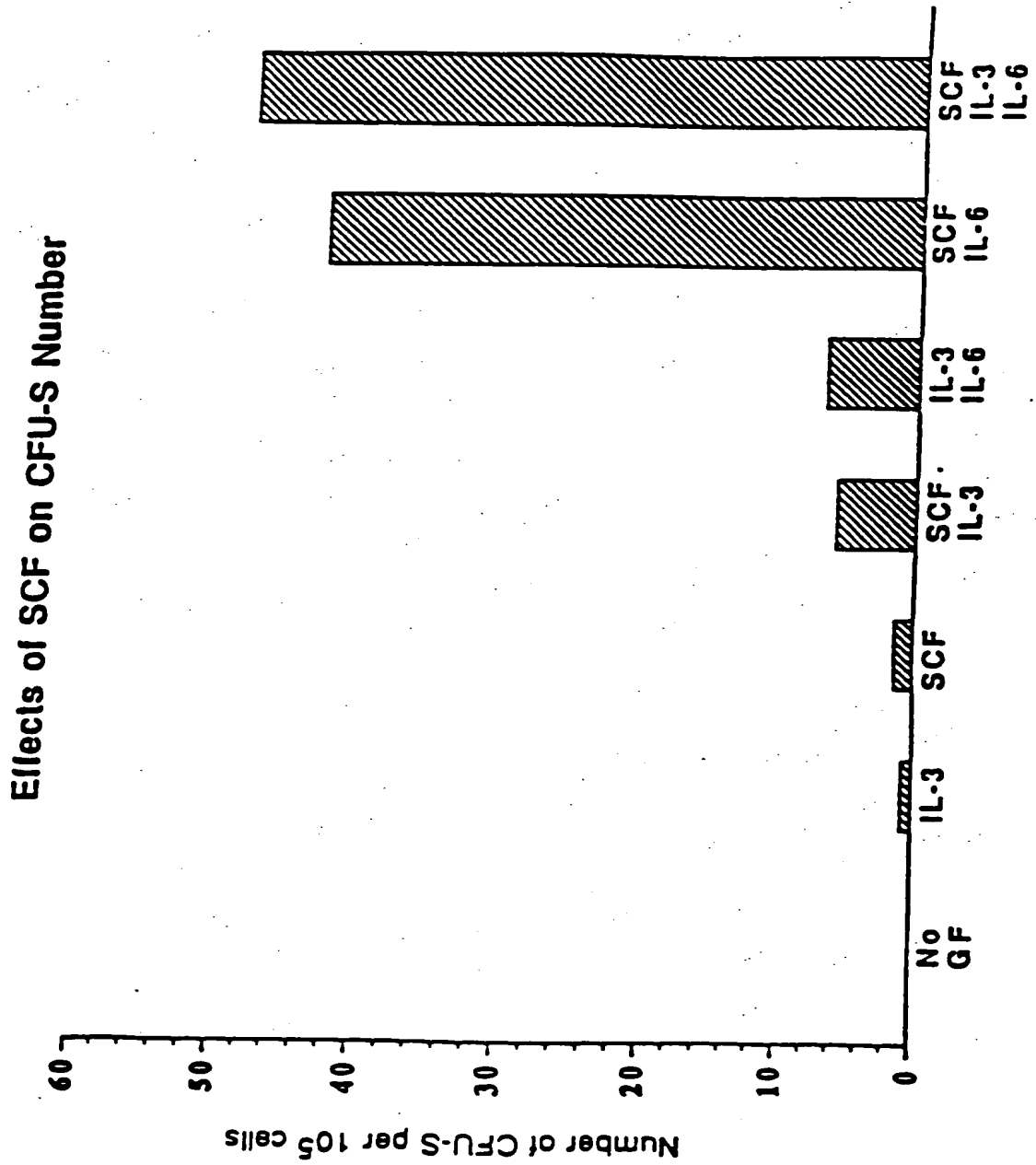


FIG. 67

EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)

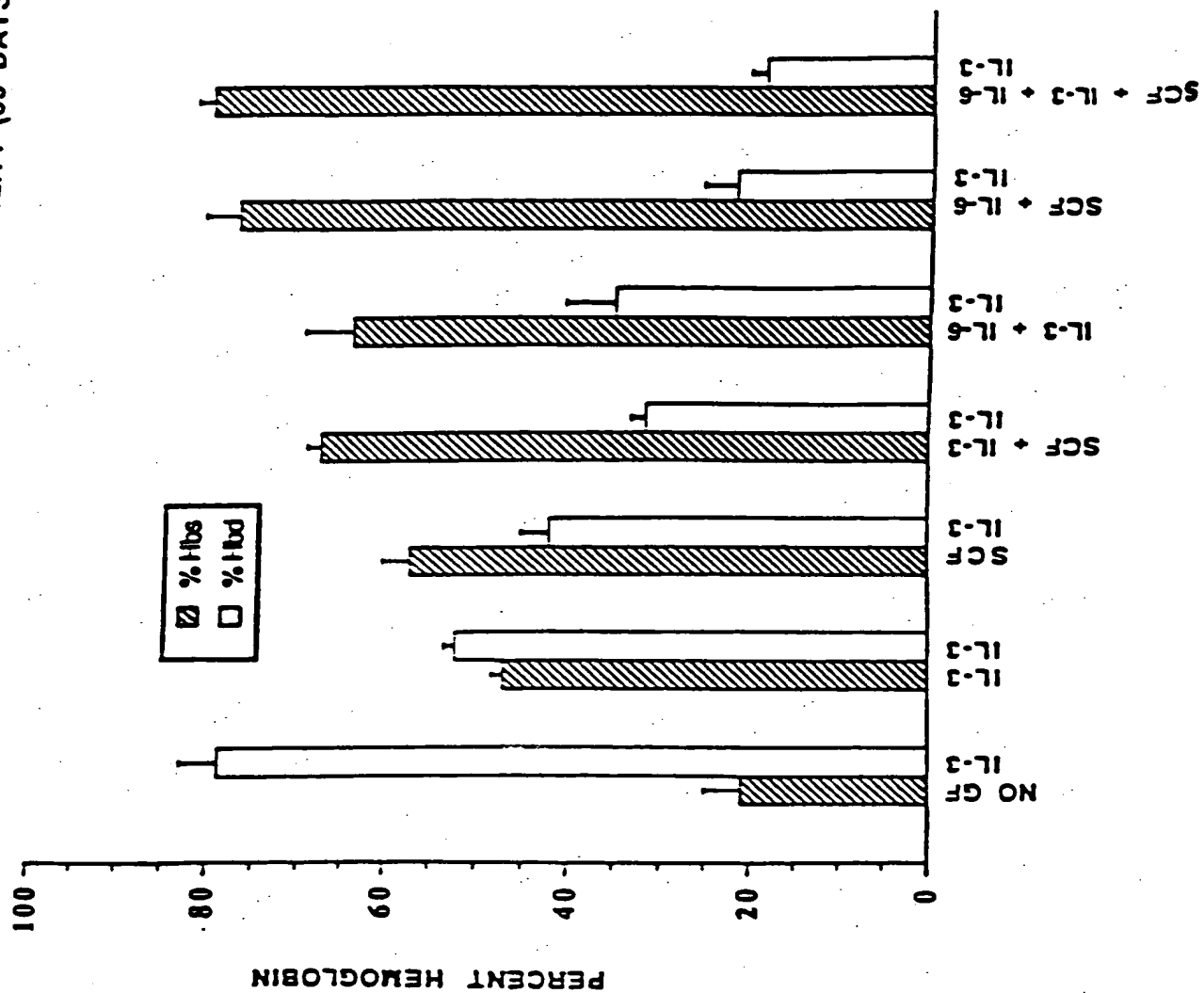


FIG. 68

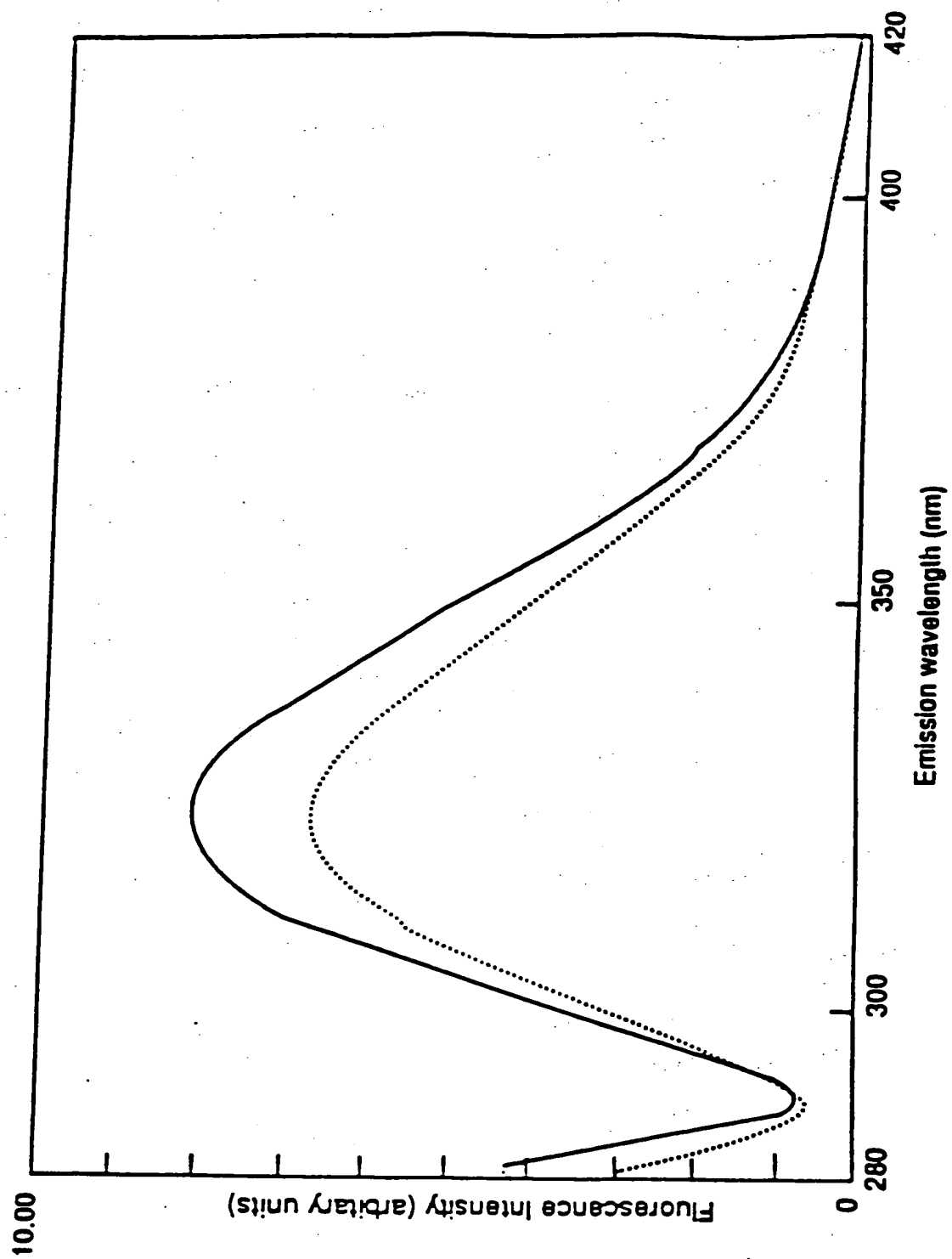


FIG. 69A

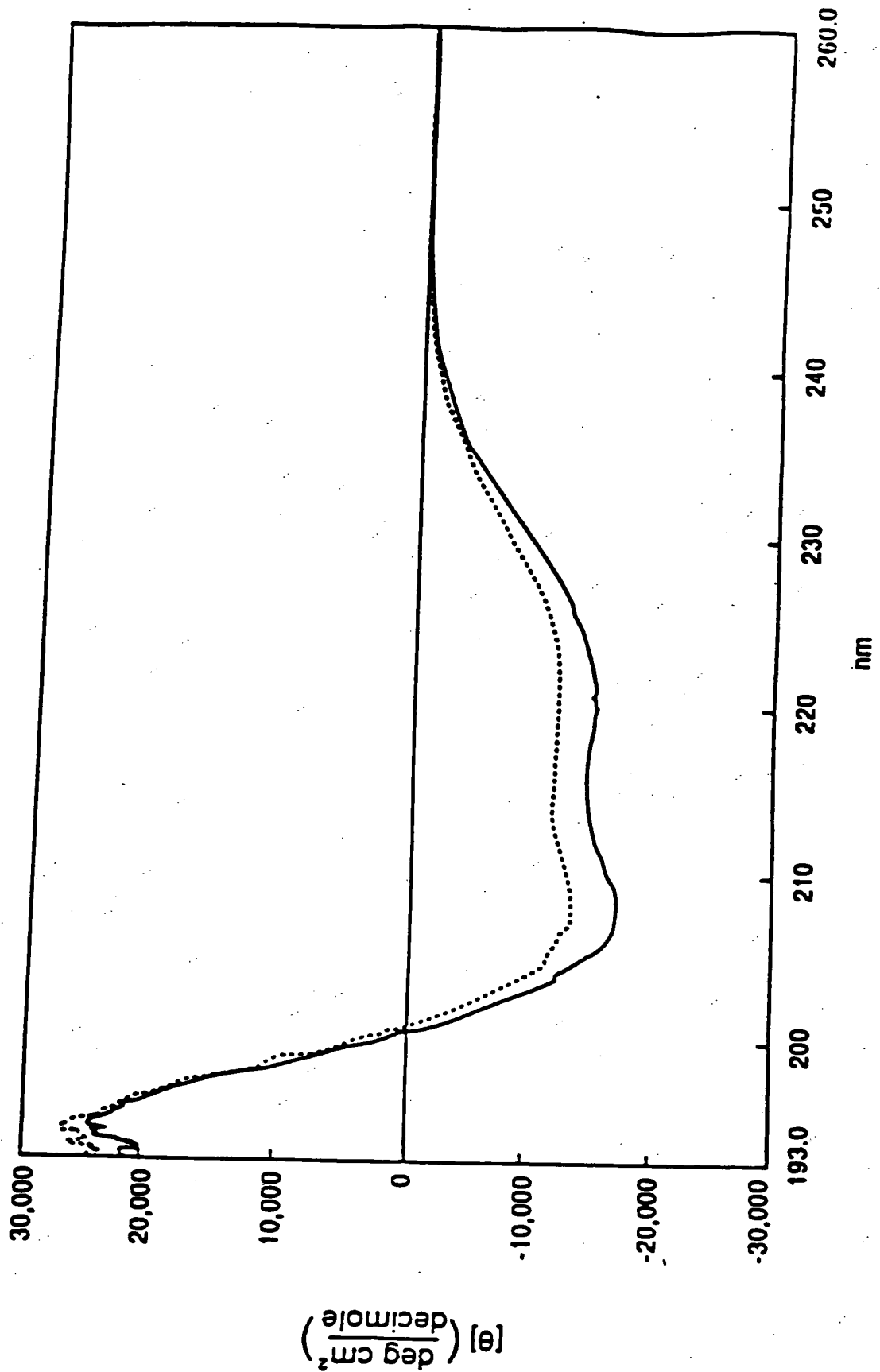


FIG. 69B

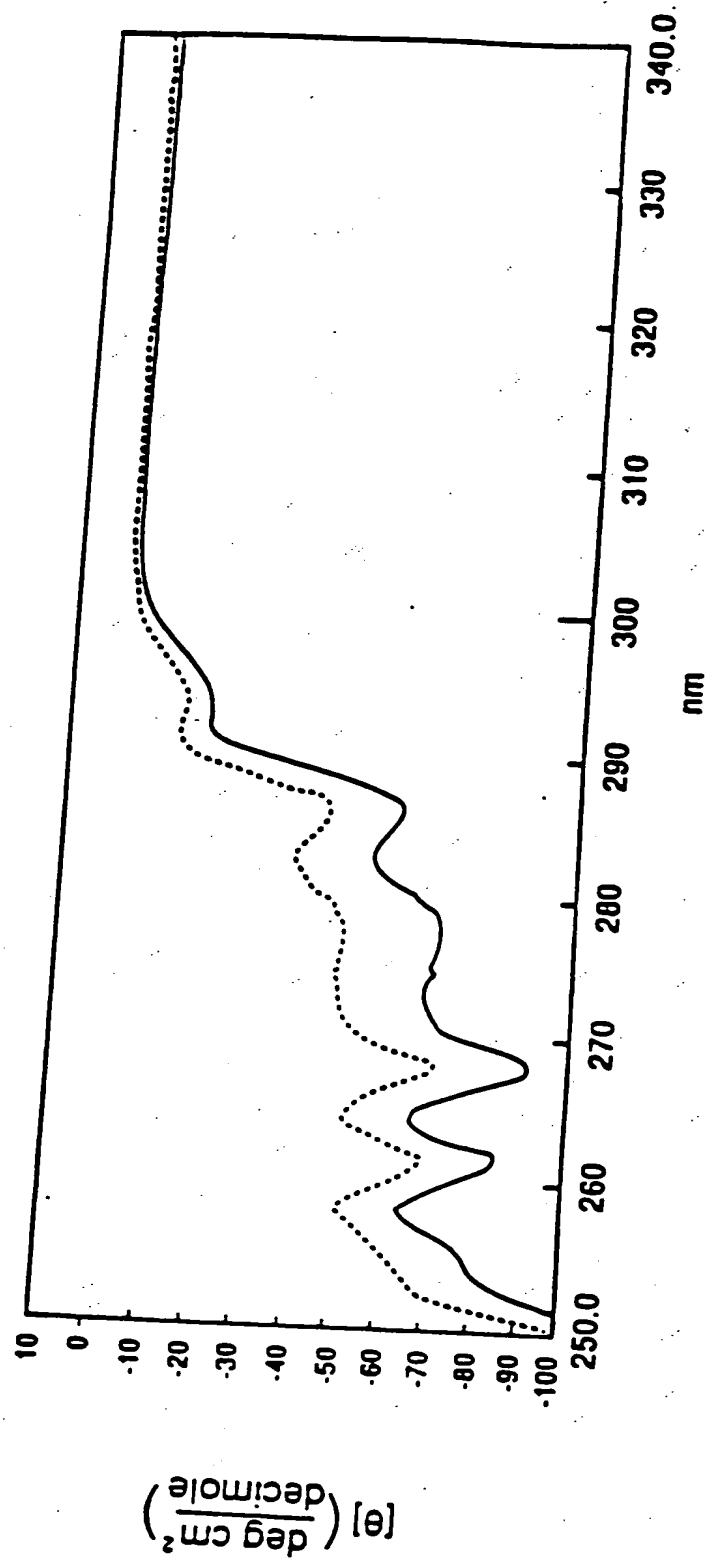


FIG. 70

